GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:30:15 ; Search time 42.1791 Seconds
(without alignments)
120.578 Million cell updates/sec

Title: US-09-641-802-3
Perfect score: 98
Sequence: 1 DQPPDVEKPDLQPFQVQS 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 422553

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	98	100.0	18	4	AAB72502	Aab72502 Colostrin
2	98	100.0	18	4	AAB59325	Aab59325 Ewe colos
3	98	100.0	18	4	AAB72248	Aab72248 Colostrin
4	98	100.0	18	4	AAB72534	Aab72534 Colostrin
5	98	100.0	18	5	AAO14579	Aao14579 Neural ce
6	98	100.0	18	5	AAM51038	Aam51038 Colostrin
7	98	100.0	18	5	AAE20230	Aae20230 Colostrin
8	41	41.8	15	5	ABG67986	Abg67986 Human ADP
9	41	41.8	15	6	ADA24138	Ada24138 Alzheimer

10	39	39.8	16	2	AAR49858	Aar49858 Sequence
11	39	39.8	16	6	ABP83082	Abp83082 G protein
12	36	36.7	15	5	AAM47777	Aam47777 Short cha
13	35	35.7	12	5	ABG67771	Abg67771 Human ADP
14	35	35.7	12	6	ADA23910	Ada23910 Alzheimer
15	35	35.7	13	3	AAB26624	Aab26624 Partial s
16	34	34.7	13	5	ABB97740	Abb97740 Human pro
17	34	34.7	13	5	ABB97739	Abb97739 Human pro
18	33	33.7	15	3	AAB21134	Aab21134 Src homol
19	33	33.7	18	2	AAY41624	Aay41624 Mammalian
20	33	33.7	18	6	AAE34138	Aae34138 T-cell st
21	33	33.7	18	6	AAE34142	Aae34142 T-cell st
22	33	33.7	18	6	AAE34133	Aae34133 T-cell st
23	32	32.7	11	3	AAB21124	Aab21124 Src homol
24	32	32.7	11	3	AAB21133	Aab21133 Src homol
25	32	32.7	17	4	AAU01841	Aau01841 Wheat pep
26	32	32.7	17	4	AAU01840	Aau01840 Wheat pep
27	32	32.7	18	2	AAW38909	Aaw38909 Peptide r
28	31	31.6	10	4	AAG97089	Aag97089 Human com
29	31	31.6	11	2	AAW17451	Aaw17451 Consensus
30	31	31.6	11	5	ABP61522	Abp61522 Human KRP
31	31	31.6	15	2	AAW45819	Aaw45819 Peptide r
32	31	31.6	15	2	AAW45614	Aaw45614 Peptide r
33	31	31.6	16	2	AAW09376	Aaw09376 Proline-r
34	31	31.6	16	2	AAW09377	Aaw09377 Proline-r
35	31	31.6	17	2	AAW12220	Aaw12220 Human ace
36	31	31.6	18	2	AAW09378	Aaw09378 Proline-r
37	30.5	31.1	11	2	AAR44563	Aar44563 Encoded b
38	30	30.6	9	5	ABP55802	Abp55802 B15 class
39	30	30.6	9	5	ABG96846	Abg96846 Human leu
40	30	30.6	9	5	ABG96954	Abg96954 Human leu
41	30	30.6	9	5	ABG96698	Abg96698 Human leu
42	30	30.6	11	7	ADC35017	Adc35017 Rho-like
43	30	30.6	13	5	ABB97741	Abb97741 Human pro
44	30	30.6	15	4	AAG88540	Aag88540 HER2/NEU
45	30	30.6	15	6	ABR30154	Abr30154 Human can
46	30	30.6	15	7	ADE70385	Ade70385 Human 161
47	30	30.6	15	7	ADE70790	Ade70790 Human 161
48	30	30.6	15	7	ADE70192	Ade70192 Human 161
49	30	30.6	17	4	AAU01833	Aau01833 Wheat Gli
50	30	30.6	17	4	AAU01822	Aau01822 Wheat Gli
51	29.5	30.1	18	3	AAY79501	Aay79501 Eimeria t
52	29	29.6	8	5	AAU82343	Aau82343 Human pap
53	29	29.6	9	5	ABG69555	Abg69555 Human CRP
54	29	29.6	10	2	AAR10268	Aar10268 Human ven
55	29	29.6	10	4	AAG96833	Aag96833 Human com
56	29	29.6	10	6	ABU90826	Abu90826 Peptide #
57	29	29.6	10	7	ADE70033	Ade70033 Human 161
58	29	29.6	11	3	AAB21127	Aab21127 Src homol
59	29	29.6	13	5	ABJ01202	Abj01202 Human Sox
60	29	29.6	15	1	AAP50841	Aap50841 Sequence
61	29	29.6	15	1	AAP82092	Aap82092 HRV2-deri
62	29	29.6	15	3	AAY93323	Aay93323 Antigenic
63	29	29.6	15	6	ABR30262	Abr30262 Human can
64	29	29.6	15	6	ABR30229	Abr30229 Human can
65	29	29.6	15	7	ADB67139	Adb67139 Human rhi
66	29	29.6	15	7	ADC35688	Adc35688 Peptide e

67	29	29.6	17	6	ABP82697	Abp82697 G protein
68	29	29.6	18	4	AAG98704	Aag98704 Human cel
69	28	28.6	9	6	ABU75492	Abu75492 Novel pro
70	28	28.6	9	6	ABU72741	Abu72741 Novel pro
71	28	28.6	9	6	ABU76002	Abu76002 Novel pro
72	28	28.6	9	6	ABU74930	Abu74930 Novel pro
73	28	28.6	9	6	ABU76707	Abu76707 Novel pro
74	28	28.6	9	6	ABU73368	Abu73368 Novel pro
75	28	28.6	10	6	ABU77821	Abu77821 Novel pro
76	28	28.6	10	6	ABU73000	Abu73000 Novel pro
77	28	28.6	10	6	ABU74640	Abu74640 Novel pro
78	28	28.6	10	6	ABU73612	Abu73612 Novel pro
79	28	28.6	10	6	ABU75215	Abu75215 Novel pro
80	28	28.6	10	6	ABU74135	Abu74135 Novel pro
81	28	28.6	10	6	ABU77684	Abu77684 Novel pro
82	28	28.6	10	6	ABU76282	Abu76282 Novel pro
83	28	28.6	11	5	AAE18843	Aae18843 Human cal
84	28	28.6	12	2	AAW16014	Aaw16014 Peptide c
85	28	28.6	12	2	AAW16260	Aaw16260 Peptide c
86	28	28.6	12	2	AAW16004	Aaw16004 Peptide c
87	28	28.6	12	2	AAW68652	Aaw68652 Random pe
88	28	28.6	12	2	AAW68884	Aaw68884 Peptide b
89	28	28.6	12	2	AAW68643	Aaw68643 Random pe
90	28	28.6	12	2	AAW58122	Aaw58122 T6 interl
91	28	28.6	12	2	AAW58364	Aaw58364 Interleuk
92	28	28.6	12	2	AAW58131	Aaw58131 T6 interl
93	28	28.6	12	2	AAY09775	Aay09775 Interleuk
94	28	28.6	12	2	AAY09766	Aay09766 Interleuk
95	28	28.6	12	2	AAY10036	Aay10036 Interleuk
96	28	28.6	12	3	AAB17854	Aab17854 IL-1 anta
97	28	28.6	12	3	AAB17569	Aab17569 IL-1 anta
98	28	28.6	12	3	AAB17579	Aab17579 IL-1 anta
99	28	28.6	12	5	ABB72465	Abb72465 Interleuk
100	28	28.6	12	5	ABB72745	Abb72745 Interleuk

ALIGNMENTS

RESULT 1
AAB72502
ID AAB72502 standard; peptide; 18 AA.
XX
AC AAB72502;
XX
DT 09-MAY-2001 (first entry)
XX
DE Colostrinin peptide #3.
XX
KW Dermatological; oxidative stress regulator; colostrinin.
XX
OS Unidentified.
XX
PN WO200112650-A2.
XX
PD 22-FEB-2001.
XX

PF 17-AUG-2000; 2000WO-US022665.
XX
PR 17-AUG-1999; 99US-0149310P.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Stanton GJ, Hughes TK, Boldogh I;
XX
DR WPI; 2001-218342/22.
XX
PT Modulating oxidative stress level in a cell, involves contacting the cell
PT with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations.
XX
PS Claim 6; Page 25; 48pp; English.
XX
CC The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidising species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient
XX
SQ Sequence 18 AA;

  Query Match   100.0%; Score 98; DB 4; Length 18;
  Best Local Similarity   100.0%; Pred. No. 2.8e-07;
  Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 DQPPDVEKPDLQPFQVQS 18
              ||||||||||||||||||
Db   1 DQPPDVEKPDLQPFQVQS 18

RESULT 2
AAB59325
ID AAB59325 standard; peptide; 18 AA.
XX
AC AAB59325;
XX
DT 21-MAR-2001 (first entry)
XX
DE Ewe colostrinin peptide fragment B-10.
XX
KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
OS Ovis sp.
XX
PN WO200075173-A2.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-GB002128.
XX
PR 02-JUN-1999; 99GB-00012852.

XX
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
PI Georgiades JA;
XX
DR WPI; 2001-071058/08.
XX
PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system and
PT immune system, viral and bacterial infections, and diseases characterized
PT by amyloid plaques.
XX
PS Claim 7; Page 27; 63pp; English.
XX
CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLQPFQVQS 18
||||||||||||||||||
Db 1 DQPPDVEKPDLQPFQVQS 18

RESULT 3
AAB72248
ID AAB72248 standard; peptide; 18 AA.
XX
AC AAB72248;
XX
DT 14-MAY-2001 (first entry)
XX
DE Colostrinin derived cytokine inducing peptide SEQ ID 3.
XX
KW Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological diosrder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.
XX
OS Synthetic.
XX
PN WO200111937-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US022818.
XX

PR 17-AUG-1999; 99US-0149311P.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX
DR WPI; 2001-202804/20.
XX
PT Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostrinin as an immunological
PT regulator.
XX
PS Claim 1; Page 34; 50pp; English.
XX
CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
CC a proline rich polypeptide aggregate contained in colostrum. The peptides
CC have immune response modulatory activity, and are capable of inducing
CC cytokines. Colostrinin and its derived peptides are useful for inducing
CC cytokine production, for modulating an immunological response and for
CC inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies
XX
SQ Sequence 18 AA;

  Query Match   100.0%; Score 98; DB 4; Length 18;
  Best Local Similarity   100.0%; Pred. No. 2.8e-07;
  Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 DQPPDVEKPDLQPFQVQS 18
              ||||||||||||||||||
Db   1 DQPPDVEKPDLQPFQVQS 18

RESULT 4
AAB72534
ID AAB72534 standard; peptide; 18 AA.
XX
AC AAB72534;
XX
DT 09-MAY-2001 (first entry)
XX
DE Colostrinin peptide #3.
XX
KW Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrum.
XX
OS Unidentified.
XX
PN WO200112651-A2.
XX
PD 22-FEB-2001.

XX
PF 17-AUG-2000; 2000WO-US022774.
XX
PR 17-AUG-1999; 99US-0149633P.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Boldogh I;
XX
DR WPI; 2001-226545/23.
XX
PT Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating damaged
PT neural cells in a patient.
XX
PS Claim 6; Page 21; 35pp; English.
XX
CC The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum
XX
SQ Sequence 18 AA;

  Query Match   100.0%; Score 98; DB 4; Length 18;
  Best Local Similarity   100.0%; Pred. No. 2.8e-07;
  Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 DQPPDVEKPDLQPFQVQS 18
              ||||||||||||||||||
Db   1 DQPPDVEKPDLQPFQVQS 18

RESULT 5
AAO14579
ID AAO14579 standard; peptide; 18 AA.
XX
AC AAO14579;
XX
DT 27-MAY-2002 (first entry)
XX
DE Neural cell regulatory colostrinin peptide 3.
XX
KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
KW neural cell treatment.
XX
OS Unidentified.
XX
FH Key   Location/Qualifiers
FT Modified-site   18
FT   /note= "Optional C-terminal amide"
XX
PN WO200213851-A1.
XX
PD 21-FEB-2002.
XX

PF 17-AUG-2000; 2000WO-US022777.
XX
PR 17-AUG-2000; 2000WO-US022777.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Boldogh I, Stanton JG, Hughes TK;
XX
DR WPI; 2002-269152/31.
XX
PT Promoting cell differentiation in a patient involves use of blood cell
PT regulator selected from colostrinin, its constituent peptide and/or
PT analog.
XX
PS Claim 7; Page 21; 37pp; English.
XX
CC The invention comprises a method for promoting cell differentiation (e.g.
CC neural cell differentiation). The method involves contacting cells with a
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
CC cells in morphology to form neural cells. Colostrinin is a proline-rich
CC polypeptide aggregate that is present in colostrum. The method of the
CC invention is useful for promoting the differentiation of cells and for
CC treating damaged neural cells in a patient. The present amino acid
CC sequence represents a specifically claimed colostrinin peptide used in
CC the method of the invention
XX
SQ Sequence 18 AA;

  Query Match   100.0%; Score 98; DB 5; Length 18;
  Best Local Similarity   100.0%; Pred. No. 2.8e-07;
  Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 DQPPDVEKPDLQPFQVQS 18
              ||||||||||||||||||
Db   1 DQPPDVEKPDLQPFQVQS 18

RESULT 6
AAM51038
ID AAM51038 standard; peptide; 18 AA.
XX
AC AAM51038;
XX
DT 30-MAY-2002 (first entry)
XX
DE Colostrinin constituent peptide.
XX
KW Colostrinin; colostrum; immunomodulator; cardiovascular;
KW blood cell regulator; cytokine inducer; beta-casein; human.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Modified-site   18
FT   /note= "optional C-terminal amidation"
XX
PN WO200213849-A1.

XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US022775.
XX
PR 17-AUG-2000; 2000WO-US022775.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX
DR WPI; 2002-269150/31.
XX
PT Modulation of blood cell proliferation in a patient involves use of blood
PT cell regulator selected from colostrinin, its constituent peptide and/or
PT analog.
XX
PS Claim 1; Page 34; 54pp; English.
XX
CC The present sequence is that of a colostrinin constituent peptide that is
CC preferred for use as an immunological regulator and as a blood cell
CC regulator in claimed methods of the invention. It is classified as having
CC a beta-casein homologue precursor. Methods are claimed for: inducing a
CC cytokine in a cell by contact with an immunological regulator, where the
CC cell is present in a cell culture, a tissue, an organ or an organism, and
CC the cell is mammalian, including human; modulating an immune response in
CC a cell by contact with the immunological regulator under conditions
CC effective to induce a cytokine; modulating an immune response in a
CC patient by administering an immunological regulator under conditions
CC effective to induce a cytokine, where the immunological regulator is
CC administered topically or as part of a dietary supplement, and where the
CC immune response is specific or non specific, an interferon response or an
CC antibody response; modulating blood cell proliferation by contacting
CC blood cells with a blood cell regulator, where the blood cells are
CC present in a cell culture or an organism, are mammalian or human, and
CC where the blood cells are increased in number or differentiated; and a
CC method for modulating blood cell proliferation in a patent. A claimed
CC cytokine-inducing composition comprises a pharmaceutical carrier and an
CC active agent such as the present peptide. Cytokines induced by this
CC peptide in human leucocyte cultures include interferon-gamma, tumour
CC necrosis factor-alpha, interleukin-6 and interleukin-10. It was one of
CC the best overall inducers in almost all cytokine and blood cell
CC proliferation experiments conducted
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLQPFQVQS 18
||||||||||||||||||
Db 1 DQPPDVEKPDLQPFQVQS 18

RESULT 7

AAE20230
ID AAE20230 standard; peptide; 18 AA.
XX
AC AAE20230;
XX
DT 18-JUN-2002 (first entry)
XX
DE Colostrinin constituent peptide #3.
XX
KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnerary.
XX
OS Unidentified.
XX
FH Key   Location/Qualifiers
FT Modified-site   18
FT   /note= "Optionally C-terminal amide"
XX
PN WO200213850-A1.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US022776.
XX
PR 17-AUG-2000; 2000WO-US022776.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Stanton GJ, Hughes TK, Boldogh I;
XX
DR WPI; 2002-269151/31.
XX
PT Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog.
XX
PS Claim 6; Page 25; 51pp; English.
XX
CC The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress level
CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,
CC organ, or organism; or for treating oxidative damage to the skin of a
CC patient e.g. animal or human; to modulate oxidative stress during/ after
CC a premature birth or normal birth, preventing/delaying aging in a
CC patient, enhancing wound healing, and the reduction of side effects of
CC cosmetic procedures. The method changes the level of an oxidising species
CC in the cell, such as decreases or prevents increase in the level of
CC damage to a biomolecule of the patient selected from DNA, protein and/or
CC lipid, compared to the same conditions when the oxidative stress
CC regulator is not present. The modulation of oxidative stress results in
CC enhanced repair, regeneration, and replacement of cells, tissues and
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
CC external organs), as well as enhanced preservation of such organs for
CC transplantation, implantation, or scientific research. The present

CC sequence is a colostrinin constituent peptide
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLQPFQVQS 18
||||||||||||||||||
Db 1 DQPPDVEKPDLQPFQVQS 18

RESULT 8
ABG67986
ID ABG67986 standard; peptide; 15 AA.
XX
AC ABG67986;
XX
DT 07-OCT-2002 (first entry)
XX
DE Human ADPI tryptic digest peptide #695.
XX
KW Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;
KW Alzheimer's disease-associated feature; neuroprotective;
KW Alzheimer's disease-associated protein isoform; nootropic;
KW ADPI tryptic digest peptide.
XX
OS Homo sapiens.
XX
PN WO200246767-A2.
XX
PD 13-JUN-2002.
XX
PF 29-NOV-2001; 2001WO-GB005289.
XX
PR 08-DEC-2000; 2000US-0254431P.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAC, Parekh RB, Rohlff C;
XX
DR WPI; 2002-508575/54.
XX
PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,
PT comprises detecting Alzheimer disease-associated features or Alzheimer
PT disease-associated protein isoforms in brain tissue from the subject.
XX
PS Claim 7; Page 56; 427pp; English.
XX
CC The present invention relates to methods and compositions for the
CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in a
CC subject. The method comprises analysing a sample of brain tissue from a
CC subject by 2D electrophoresis to generate a 2D array of Alzheimer's
CC disease-associated features (ADFs), whose relative abundance correlates
CC with the presence, absence, stage or severity of AD and comparing the
CC abundance of each feature with the abundance of that chosen feature in

CC brain tissue from persons free from AD. The invention also describes
CC Alzheimer's disease-associated protein isoforms (ADPIs) detectable in
CC brain tissue. The methods and compositions of the invention are useful
CC for the screening, diagnosis or prognosis of AD in a subject, for
CC determining the stage or severity of AD in a subject, for identifying a
CC subject at risk of developing AD, or for monitoring the effect of therapy
CC administered to a subject having AD. Antibodies capable of binding to
CC ADPIs are useful for treating or preventing AD, and for determining the
CC efficacy of a given treatment regime. An agent that modulates the
CC activity of ADPI is useful in the manufacture of a medicament for the
CC treatment or prevention of AD in a subject. ABG67292-ABG68038 represent
CC human ADPI tryptic digest peptides
XX
SQ Sequence 15 AA;

Query Match 41.8%; Score 41; DB 5; Length 15;
Best Local Similarity 47.1%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 0; Indels 6; Gaps 1;

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Qy          1 DQPPDVEKPDLQPFQVQ 17
              |||||:|      ||::
Db          5 DQPPDIE------FQIR 15
```

RESULT 9
ADA24138
ID ADA24138 standard; peptide; 15 AA.
XX
AC ADA24138;
XX
DT 20-NOV-2003 (first entry)
XX
DE Alzheimer's disease-associated protein isoform tryptic peptide #747.
XX
KW human; Alzheimer's disease; vascular dementia; Lewy body dementia;
KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;
KW Alzheimer's disease-associated protein isoform; ADPI.
XX
OS Homo sapiens.
XX
PN US2003064411-A1.
XX
PD 03-APR-2003.
XX
PF 10-DEC-2001; 2001US-00014340.
XX
PR 08-DEC-2000; 2000US-0254431P.
XX
PA (HERA/) HERATH H M A C.
PA (PARE/) PAREKH R B.
PA (ROHL/) ROHLFF C.
XX
PI Herath HMAC, Parekh RB, Rohlff C;
XX
DR WPI; 2003-540784/51.
XX
PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,

PT involves analyzing test sample of brain tissue from subject, and
PT comparing feature in test sample with that of person(s) free from
PT Alzheimer's disease.
XX
PS Disclosure; SEQ ID NO 747; 115pp; English.
XX
CC The invention relates to a method of screening or diagnosing Alzheimer's
CC disease in a subject. The method is useful for screening, diagnosis or
CC prognosis of Alzheimer's disease in a subject for determining the stage
CC of severity of Alzheimer's disease in a subject, for identifying a
CC subject at risk of developing Alzheimer's disease, or for monitoring the
CC effect of therapy administered to a subject having Alzheimer's disease.
CC The method is also useful in treating vascular dementia, Lewy body
CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or
CC depression. The inventive method identifies sensitive and specific
CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.
CC It provides therapeutic agents for Alzheimer's disease that works
CC quickly, potently, specifically with fewer side effects. The present
CC sequence represents the amino acid sequence of a Alzheimer's disease-
CC associated protein isoform tryptic peptide.
XX
SQ Sequence 15 AA;

Query Match 41.8%; Score 41; DB 6; Length 15;
Best Local Similarity 47.1%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 0; Indels 6; Gaps 1;

```
Qy          1 DQPPDVEKPDLQPFQVQ 17
              |||||:|      ||::
Db          5 DQPPDIE------FQIR 15
```

RESULT 10
AAR49858
ID AAR49858 standard; peptide; 16 AA.
XX
AC AAR49858;
XX
DT 25-MAR-2003 (revised)
DT 12-SEP-1994 (first entry)
XX
DE Sequence of tryptic digest peptide of bovine glial growth factor III (GGF
DE III).
XX
KW Glial growth factor; GGF III; mitogen; Schwann cell.
XX
OS Bos taurus.
XX
PN WO9404560-A1.
XX
PD 03-MAR-1994.
XX
PF 13-AUG-1993; 93WO-GB001721.
XX
PR 14-AUG-1992; 92GB-00017316.
XX
PA (LUDW-) LUDWIG INST CANCER RES.

XX
PI Goodearl ADJ, Stroobant P, Waterfield MD;
XX
DR WPI; 1994-083104/10.
XX
PT New polypeptide factor and peptide(s) from bovine pituitary - having
PT mitogenic activity in stimulating division of Schwann cells, used for
PT therapy, prophylaxis, diagnosis of neuro-degenerative disease, glial cell
PT tumours, etc.
XX
PS Claim 32; Page 31; 44pp; English.
XX
CC A novel polypeptide was purified from bovine pituitaries. It has
CC mitogenic activity stimulating the division of Schwann cells, and
CC exhibits a mol. wt. of 43-35kD when carrying native glycosylation. It was
CC digested with trypsin and lysylendopeptidase to obtain novel peptides
CC AAR49858-R49866 and AAR49867-R49871 respectively. When peptides AAR49862-
CC R49866 were sequenced to completion it was found that none of these
CC sequences is apparently related to GGF-I or GGF-II peptide sequences. A
CC polypeptide contg. any of the sequences in AAR49858- AAR49871 is claimed,
CC as is DNA encoding each of the peptides. The final Lys in the sequence is
CC bracketed. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 16 AA;

Query Match 39.8%; Score 39; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 69;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          6 VEKPDLQPF 14
              : ||||:||
Db          2 ISKPDLKPF 10
```

RESULT 11
ABP83082
ID ABP83082 standard; peptide; 16 AA.
XX
AC ABP83082;
XX
DT 04-MAR-2003 (first entry)
XX
DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1755.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.
XX
OS Homo sapiens.

XX
PN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
PR 19-DEC-2000; 2000US-0257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burmer GC, Roush CL, Brown JP;
XX
DR WPI; 2003-046718/04.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX
PS Claim 1; Fig 2; 523pp; English.
XX
CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 16 AA;

Query Match 39.8%; Score 39; DB 6; Length 16;
Best Local Similarity 50.0%; Pred. No. 69;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```
Qy          2 QPPDVEKPDLQP 13
              :|||: | |  |
Db          5 RPPDIRKSDSSP 16
```

RESULT 12
AAM47777
ID AAM47777 standard; peptide; 15 AA.
XX
AC AAM47777;
XX
DT 26-FEB-2002 (first entry)
XX
DE Short chain dehydrogenase 32 peptide fragment.
XX
KW Short chain dehydrogenase 32; tumour; haemopathy; HIV infection;
KW immunological disease; inflammation; gene therapy; cytostatic;
KW haemostatic; virucide; immunomodulatory; antiinflammatory.
XX
OS Unidentified.
XX
PN CN1307114-A.
XX
PD 08-AUG-2001.
XX
PF 28-JAN-2000; 2000CN-00111584.
XX
PR 28-JAN-2000; 2000CN-00111584.
XX
PA (BODA-) BODAO GENE TECH CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-026893/04.
XX
PT New polypeptide for treating malignant tumors and HIV infection,
PT comprises the polypeptide-short chain dehydrogenase 32 and polynucleotide
PT for coding said polypeptide.
XX
PS Example 6; Page 27 (Disclosure); 33pp; Chinese.
XX
CC The present invention relates to short chain dehydrogenase 32 (AAM47776).
CC The protein and its coding sequence are useful for treating various
CC diseases, such as malignant tumours, haemopathy, HIV infection,
CC immunological diseases and inflammations. The present sequence is an N-
CC terminal peptide fragment of the protein, which was used in an example
CC from the present invention
XX
SQ Sequence 15 AA;

  Query Match   36.7%; Score 36; DB 5; Length 15;
  Best Local Similarity   63.6%; Pred. No. 1.7e+02;
  Matches   7; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy   3 PPDVEKPDLQP 13
              ||||| | |
Db   5 PPDVEGDDCLP 15

RESULT 13

ABG67771
ID ABG67771 standard; peptide; 12 AA.
XX
AC ABG67771;
XX
DT 07-OCT-2002 (first entry)
XX
DE Human ADPI tryptic digest peptide #480.
XX
KW Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;
KW Alzheimer's disease-associated feature; neuroprotective;
KW Alzheimer's disease-associated protein isoform; nootropic;
KW ADPI tryptic digest peptide.
XX
OS Homo sapiens.
XX
PN WO200246767-A2.
XX
PD 13-JUN-2002.
XX
PF 29-NOV-2001; 2001WO-GB005289.
XX
PR 08-DEC-2000; 2000US-0254431P.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAC, Parekh RB, Rohlff C;
XX
DR WPI; 2002-508575/54.
XX
PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,
PT comprises detecting Alzheimer disease-associated features or Alzheimer
PT disease-associated protein isoforms in brain tissue from the subject.
XX
PS Claim 7; Page 55; 427pp; English.
XX
CC The present invention relates to methods and compositions for the
CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in a
CC subject. The method comprises analysing a sample of brain tissue from a
CC subject by 2D electrophoresis to generate a 2D array of Alzheimer's
CC disease-associated features (ADFs), whose relative abundance correlates
CC with the presence, absence, stage or severity of AD and comparing the
CC abundance of each feature with the abundance of that chosen feature in
CC brain tissue from persons free from AD. The invention also describes
CC Alzheimer's disease-associated protein isoforms (ADPIs) detectable in
CC brain tissue. The methods and compositions of the invention are useful
CC for the screening, diagnosis or prognosis of AD in a subject, for
CC determining the stage or severity of AD in a subject, for identifying a
CC subject at risk of developing AD, or for monitoring the effect of therapy
CC administered to a subject having AD. Antibodies capable of binding to
CC ADPIs are useful for treating or preventing AD, and for determining the
CC efficacy of a given treatment regime. An agent that modulates the
CC activity of ADPI is useful in the manufacture of a medicament for the
CC treatment or prevention of AD in a subject. ABG67292-ABG68038 represent
CC human ADPI tryptic digest peptides
XX
SQ Sequence 12 AA;

Query Match 35.7%; Score 35; DB 5; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy          3 PPDVEKPDLQ 12
              ||  | |||:
Db          3 PPSAEYPDLR 12
```

RESULT 14
ADA23910
ID ADA23910 standard; peptide; 12 AA.
XX
AC ADA23910;
XX
DT 20-NOV-2003 (first entry)
XX
DE Alzheimer's disease-associated protein isoform tryptic peptide #519.
XX
KW human; Alzheimer's disease; vascular dementia; Lewy body dementia;
KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;
KW Alzheimer's disease-associated protein isoform; ADPI.
XX
OS Homo sapiens.
XX
PN US2003064411-A1.
XX
PD 03-APR-2003.
XX
PF 10-DEC-2001; 2001US-00014340.
XX
PR 08-DEC-2000; 2000US-0254431P.
XX
PA (HERA/) HERATH H M A C.
PA (PARE/) PAREKH R B.
PA (ROHL/) ROHLFF C.
XX
PI Herath HMAC, Parekh RB, Rohlff C;
XX
DR WPI; 2003-540784/51.
XX
PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,
PT involves analyzing test sample of brain tissue from subject, and
PT comparing feature in test sample with that of person(s) free from
PT Alzheimer's disease.
XX
PS Disclosure; SEQ ID NO 519; 115pp; English.
XX
CC The invention relates to a method of screening or diagnosing Alzheimer's
CC disease in a subject. The method is useful for screening, diagnosis or
CC prognosis of Alzheimer's disease in a subject for determining the stage
CC of severity of Alzheimer's disease in a subject, for identifying a
CC subject at risk of developing Alzheimer's disease, or for monitoring the
CC effect of therapy administered to a subject having Alzheimer's disease.
CC The method is also useful in treating vascular dementia, Lewy body
CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or

CC depression. The inventive method identifies sensitive and specific
CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.
CC It provides therapeutic agents for Alzheimer's disease that works
CC quickly, potently, specifically with fewer side effects. The present
CC sequence represents the amino acid sequence of a Alzheimer's disease-
CC associated protein isoform tryptic peptide.
XX
SQ Sequence 12 AA;

Query Match 35.7%; Score 35; DB 6; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy          3 PPDVEKPDLQ 12
              ||  | |||:
Db          3 PPSAEYPDLR 12
```

RESULT 15
AAB26624
ID AAB26624 standard; peptide; 13 AA.
XX
AC AAB26624;
XX
DT 22-JAN-2001 (first entry)
XX
DE Partial sequence #24 of Breast Cancer-Associated Protein Isoform.
XX
KW BPI; breast cancer-associated protein isoform; gene therapy;
KW breast cancer.
XX
OS Homo sapiens.
XX
PN WO200055628-A1.
XX
PD 21-SEP-2000.
XX
PF 13-MAR-2000; 2000WO-GB000908.
XX
PR 12-MAR-1999; 99GB-00005817.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Amess B, Townsend RR, Parekh RB, Waterfield MD, O'hare MJ;
XX
DR WPI; 2000-602142/57.
XX
PT Screening, diagnosis of breast cancer and monitoring the effectiveness of
PT breast cancer therapy, involves detecting breast cancer-associated
PT features and breast cancer-associated protein isoforms.
XX
PS Disclosure; Page 14; 86pp; English.
XX
CC The present invention relates to the screening, diagnosis and prognosis
CC of breast cancer, for monitoring the effectiveness of breast cancer
CC treatment in a human, comprising identifying the presence or absence of
CC breast cancer-associated features (BF) or breast cancer-associated

CC protein isoforms (BPIs). Antibodies derived from BF and BPIs may be
CC useful for the treatment and screening of breast cancer, in particular
CC metastatic breast cancer. The present sequence is the partial sequence of
CC a BPI
XX
SQ Sequence 13 AA;

Query Match 35.7%; Score 35; DB 3; Length 13;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy          3 PPDVEKPDLQ 12
              ||  | |||:
Db          4 PPSAEYPDLR 13
```

RESULT 16
ABB97740
ID ABB97740 standard; peptide; 13 AA.
XX
AC ABB97740;
XX
DT 11-JUL-2002 (first entry)
XX
DE Human procathepsin W epitope peptide #120.
XX
KW Human; procathepsin W; cathepsin W; monoclonal antibody; epitope.
XX
OS Homo sapiens.
XX
PN WO200226831-A1.
XX
PD 04-APR-2002.
XX
PF 09-JUL-2001; 2001WO-EP007877.
XX
PR 29-SEP-2000; 2000DE-01048727.
XX
PA (LABS-) LABSOFT DIAGNOSTICS AG.
XX
PI Weber E;
XX
DR WPI; 2002-330095/36.
XX
PT New hybridoma cell lines that produces antibodies specific for human
PT cathepsin W, useful e.g. for diagnosis, therapy and drug targeting.
XX
PS Disclosure; Fig 1; 23pp; German.
XX
CC The present invention relates to hybridoma cell lines that produce
CC monoclonal antibodies directed against a defined epitope of human
CC (pro)cathepsin W, which are produced by fusing myeloma cells with spleen
CC cells from an animal that has been immunised with recombinant
CC procathepsin W. The antibodies produced are useful for analysis,
CC diagnosis (detection of human (pro)cathepsin W), purification of
CC (pro)cathepsin W (also for clarifying processing of the precursor and
CC functional significance of the mature protein), for drug targeting and

CC for therapeutic use. The present sequence is an epitope of human
CC procathepsin W
XX
SQ Sequence 13 AA;

Query Match 34.7%; Score 34; DB 5; Length 13;
Best Local Similarity 62.5%; Pred. No. 2.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy          6 VEKPDLQP 13
              |:|||::|
Db          3 VQKPDMKP 10
```

RESULT 17
ABB97739
ID ABB97739 standard; peptide; 13 AA.
XX
AC ABB97739;
XX
DT 11-JUL-2002 (first entry)
XX
DE Human procathepsin W epitope peptide #119.
XX
KW Human; procathepsin W; cathepsin W; monoclonal antibody; epitope.
XX
OS Homo sapiens.
XX
PN WO200226831-A1.
XX
PD 04-APR-2002.
XX
PF 09-JUL-2001; 2001WO-EP007877.
XX
PR 29-SEP-2000; 2000DE-01048727.
XX
PA (LABS-) LABSOFT DIAGNOSTICS AG.
XX
PI Weber E;
XX
DR WPI; 2002-330095/36.
XX
PT New hybridoma cell lines that produces antibodies specific for human
PT cathepsin W, useful e.g. for diagnosis, therapy and drug targeting.
XX
PS Disclosure; Fig 1; 23pp; German.
XX
CC The present invention relates to hybridoma cell lines that produce
CC monoclonal antibodies directed against a defined epitope of human
CC (pro)cathepsin W, which are produced by fusing myeloma cells with spleen
CC cells from an animal that has been immunised with recombinant
CC procathepsin W. The antibodies produced are useful for analysis,
CC diagnosis (detection of human (pro)cathepsin W), purification of
CC (pro)cathepsin W (also for clarifying processing of the precursor and
CC functional significance of the mature protein), for drug targeting and
CC for therapeutic use. The present sequence is an epitope of human
CC procathepsin W

XX
SQ Sequence 13 AA;

Query Match 34.7%; Score 34; DB 5; Length 13;
Best Local Similarity 62.5%; Pred. No. 2.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy          6 VEKPDLQP 13
              |:|||::|
Db          6 VQKPDMKP 13
```

RESULT 18
AAB21134
ID AAB21134 standard; peptide; 15 AA.
XX
AC AAB21134;
XX
DT 19-JAN-2001 (first entry)
XX
DE Src homology 3 domain binding peptide #11.
XX
KW Src homology domain 3; SH3; protein-protein interaction; cancer;
KW signal transduction inhibition; immune suppression-associated disease.
XX
OS Synthetic.
XX
PN WO200047607-A1.
XX
PD 17-AUG-2000.
XX
PF 12-FEB-2000; 2000WO-KR000107.
XX
PR 12-FEB-1999; 99AU-00008643.
PR 02-JUN-1999; 99KR-00020282.
XX
PA (YOON/) YOON J H.
PA (HANY/) HAN Y T.
XX
PI Yoon JH, Han YT, Lee KY;
XX
DR WPI; 2000-533010/48.
XX
PT Synthetic peptides useful for treating cancers and immunosuppressive
PT disorders by disrupting interactions of the SH (Src homology) 2 and SH3
PT motifs of Src family kinase proteins.
XX
PS Claim 3; Page 35; 40pp; English.
XX
CC The present sequence is a synthetic peptide which has a high affinity for
CC the src homology 3 (SH3) domain of protein kinases. Protein kinases are
CC involved in signal transduction pathways, and this peptide can be used to
CC inhibit these, by disrupting protein-protein interactions, in the
CC treatment of cancer, particularly hepatocellular carcinoma, cervical
CC cancer, colon adenocarcinoma and fibrosarcoma, and immune suppression-
CC associated diseases
XX

SQ Sequence 15 AA;

Query Match 33.7%; Score 33; DB 3; Length 15;
Best Local Similarity 41.7%; Pred. No. 4.7e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 DQPPDVEKPDLQ 12
              ::|| |  || :
Db          2 ERPPPVPNPDYE 13
```

RESULT 19
AAY41624
ID AAY41624 standard; peptide; 18 AA.
XX
AC AAY41624;
XX
DT 02-DEC-1999 (first entry)
XX
DE Mammalian ion channel proline rich motif containing peptide #18.
XX
KW SH3 domain; binding motif; potassium channel; protein tyrosine kinase;
KW proline rich.
XX
OS Rattus sp.
XX
PN US5955259-A.
XX
PD 21-SEP-1999.
XX
PF 19-DEC-1996; 96US-00769745.
XX
PR 19-DEC-1996; 96US-00769745.
XX
PA (UYBR-) UNIV BRANDEIS.
XX
PI Holmes TC, Levitan IB;
XX
DR WPI; 1999-560490/47.
XX
PT Identification of compounds that modulate potassium ion channel binding
PT with protein tyrosine kinase SH3 domains.
XX
PS Disclosure; Col 8; 18pp; English.
XX
CC A method has been developed for determining if a compound modulates the
CC binding of a potassium ion channel to the SH3 domain of a protein
CC tyrosine kinase by contacting the channel with a polypeptide comprising
CC the SH3 domain and the compound to be assessed and measuring channel-SH3
CC binding. The method is useful for assessing the ability of a compound to
CC modulate the formation of channel-SH3 domain complexes to improve the
CC understanding of mechanisms of potassium channel blockage and asses the
CC ability of potential therapeutics to inhibit blockage. AAY41607 to
CC AAY41644 represent mammalian ion channel peptides with proline-rich
CC motifs
XX
SQ Sequence 18 AA;

Query Match 33.7%; Score 33; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```
Qy          2 QPPDVEKPDLQP 13
              |||:   | | |
Db          6 QPPESSPPPLLP 17
```

RESULT 20
AAE34138
ID AAE34138 standard; peptide; 18 AA.
XX
AC AAE34138;
XX
DT 02-MAY-2003 (first entry)
XX
DE T-cell stimulatory gluten peptide #17.
XX
KW Human leukocyte antigen; HLA; T-cell receptor; giardiasis; celiac sprue;
KW food-related immune enteropathy; tropical sprue; gluten sensitivity;
KW food allergy; protozoacide; antiinflammatory; immunosuppressive; gluten.
XX
OS Unidentified.
XX
PN WO200283722-A2.
XX
PD 24-OCT-2002.
XX
PF 11-APR-2002; 2002WO-NL000235.
XX
PR 12-APR-2001; 2001EP-00201377.
PR 16-NOV-2001; 2001EP-00204383.
XX
PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
XX
PI Drijfhout JW, Koning F, Mcadam SN, Sollid LM;
XX
DR WPI; 2003-093000/08.
XX
PT Novel isolated or recombinant human leukocyte antigen-DQ restricted T-
PT cell receptor for treating food-related immune enteropathy such as celiac
PT sprue, tropical sprue, giardiasis and food allergies of childhood.
XX
PS Disclosure; Fig 2; 64pp; English.
XX
CC The present invention relates to novel isolated or recombinant human
CC leukocyte antigen (HLA)-DQ restricted T-cell receptor or its functional
CC equivalent and/or fragment, capable of recognising a prolamine-derived
CC peptide. The invention relates to recombinant or synthetic prolamine
CC derived peptides involved in food-related immune enteropathy. The
CC pharmaceutical composition is useful to treat food-related immune
CC enteropathies such as celiac sprue, tropical sprue, giardiasis or food
CC allergies of childhood. It is useful to induce tolerance, treat gluten-
CC sensitivity and to eliminate gluten-sensitive T-cells. Sequences of the
CC invention are useful to decrease the amount of toxic prolamine-derived

CC peptides in food or food components and to select and/or breed a cereal.
CC The cereal is useful for inclusion in a diet for a gluten sensitive
CC individual. Blocking substances are useful to decrease the binding of HLA
CC -DQ restricted T-cell receptor to a prolamine-derived peptide involved in
CC food-related immune enteropathy for depletion of T-cells bearing the HLA-
CC DQ restricted T-cell receptor. The present sequence is T-cell stimulatory
CC gluten peptide. This sequence is used in the invention
XX
SQ Sequence 18 AA;

Query Match 33.7%; Score 33; DB 6; Length 18;
Best Local Similarity 46.7%; Pred. No. 5.6e+02;
Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```
Qy          3 PPDVEKPDLQPFQVQ 17
              ||    |  |||  |
Db          2 PPQQPYPQPQPFPSQ 16
```

RESULT 21
AAE34142
ID AAE34142 standard; peptide; 18 AA.
XX
AC AAE34142;
XX
DT 02-MAY-2003 (first entry)
XX
DE T-cell stimulatory gluten peptide #21.
XX
KW Human leukocyte antigen; HLA; T-cell receptor; giardiasis; celiac sprue;
KW food-related immune enteropathy; tropical sprue; gluten sensitivity;
KW food allergy; protozoacide; antiinflammatory; immunosuppressive; gluten.
XX
OS Unidentified.
XX
PN WO200283722-A2.
XX
PD 24-OCT-2002.
XX
PF 11-APR-2002; 2002WO-NL000235.
XX
PR 12-APR-2001; 2001EP-00201377.
PR 16-NOV-2001; 2001EP-00204383.
XX
PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
XX
PI Drijfhout JW, Koning F, Mcadam SN, Sollid LM;
XX
DR WPI; 2003-093000/08.
XX
PT Novel isolated or recombinant human leukocyte antigen-DQ restricted T-
PT cell receptor for treating food-related immune enteropathy such as celiac
PT sprue, tropical sprue, giardiasis and food allergies of childhood.
XX
PS Disclosure; Fig 2; 64pp; English.
XX
CC The present invention relates to novel isolated or recombinant human

CC leukocyte antigen (HLA)-DQ restricted T-cell receptor or its functional
CC equivalent and/or fragment, capable of recognising a prolamine-derived
CC peptide. The invention relates to recombinant or synthetic prolamine
CC derived peptides involved in food-related immune enteropathy. The
CC pharmaceutical composition is useful to treat food-related immune
CC enteropathies such as celiac sprue, tropical sprue, giardiasis or food
CC allergies of childhood. It is useful to induce tolerance, treat gluten-
CC sensitivity and to eliminate gluten-sensitive T-cells. Sequences of the
CC invention are useful to decrease the amount of toxic prolamine-derived
CC peptides in food or food components and to select and/or breed a cereal.
CC The cereal is useful for inclusion in a diet for a gluten sensitive
CC individual. Blocking substances are useful to decrease the binding of HLA
CC -DQ restricted T-cell receptor to a prolamine-derived peptide involved in
CC food-related immune enteropathy for depletion of T-cells bearing the HLA-
CC DQ restricted T-cell receptor. The present sequence is T-cell stimulatory
CC gluten peptide. This sequence is used in the invention
XX
SQ Sequence 18 AA;

Query Match 33.7%; Score 33; DB 6; Length 18;
Best Local Similarity 46.7%; Pred. No. 5.6e+02;
Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```
Qy          3 PPDVEKPDLQPFQVQ 17
              ||    |  |||  |
Db          2 PPQQPYPQPQPFPSQ 16
```

RESULT 22
AAE34133
ID AAE34133 standard; peptide; 18 AA.
XX
AC AAE34133;
XX
DT 02-MAY-2003 (first entry)
XX
DE T-cell stimulatory gluten peptide #12.
XX
KW Human leukocyte antigen; HLA; T-cell receptor; giardiasis; celiac sprue;
KW food-related immune enteropathy; tropical sprue; gluten sensitivity;
KW food allergy; protozoacide; antiinflammatory; immunosuppressive; gluten.
XX
OS Unidentified.
XX
PN WO200283722-A2.
XX
PD 24-OCT-2002.
XX
PF 11-APR-2002; 2002WO-NL000235.
XX
PR 12-APR-2001; 2001EP-00201377.
PR 16-NOV-2001; 2001EP-00204383.
XX
PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
XX
PI Drijfhout JW, Koning F, Mcadam SN, Sollid LM;
XX

DR WPI; 2003-093000/08.
XX
PT Novel isolated or recombinant human leukocyte antigen-DQ restricted T-
PT cell receptor for treating food-related immune enteropathy such as celiac
PT sprue, tropical sprue, giardiasis and food allergies of childhood.
XX
PS Disclosure; Fig 2; 64pp; English.
XX
CC The present invention relates to novel isolated or recombinant human
CC leukocyte antigen (HLA)-DQ restricted T-cell receptor or its functional
CC equivalent and/or fragment, capable of recognising a prolamine-derived
CC peptide. The invention relates to recombinant or synthetic prolamine
CC derived peptides involved in food-related immune enteropathy. The
CC pharmaceutical composition is useful to treat food-related immune
CC enteropathies such as celiac sprue, tropical sprue, giardiasis or food
CC allergies of childhood. It is useful to induce tolerance, treat gluten-
CC sensitivity and to eliminate gluten-sensitive T-cells. Sequences of the
CC invention are useful to decrease the amount of toxic prolamine-derived
CC peptides in food or food components and to select and/or breed a cereal.
CC The cereal is useful for inclusion in a diet for a gluten sensitive
CC individual. Blocking substances are useful to decrease the binding of HLA
CC -DQ restricted T-cell receptor to a prolamine-derived peptide involved in
CC food-related immune enteropathy for depletion of T-cells bearing the HLA-
CC DQ restricted T-cell receptor. The present sequence is T-cell stimulatory
CC gluten peptide. This sequence is used in the invention
XX
SQ Sequence 18 AA;

  Query Match   33.7%; Score 33; DB 6; Length 18;
  Best Local Similarity   46.7%; Pred. No. 5.6e+02;
  Matches   7; Conservative   0; Mismatches   8; Indels   0; Gaps   0;

Qy   3 PPDVEKPDLQPFQVQ 17
              || | ||| |
Db   2 PPQQPYPQPQPFPSQ 16

RESULT 23
AAB21124
ID AAB21124 standard; peptide; 11 AA.
XX
AC AAB21124;
XX
DT 19-JAN-2001 (first entry)
XX
DE Src homology 3 domain binding peptide #1.
XX
KW Src homology domain 3; SH3; protein-protein interaction; cancer;
KW signal transduction inhibition; immune suppression-associated disease.
XX
OS Synthetic.
XX
PN WO200047607-A1.
XX
PD 17-AUG-2000.
XX
PF 12-FEB-2000; 2000WO-KR000107.

XX
PR 12-FEB-1999; 99AU-00008643.
PR 02-JUN-1999; 99KR-00020282.
XX
PA (YOON/) YOON J H.
PA (HANY/) HAN Y T.
XX
PI Yoon JH, Han YT, Lee KY;
XX
DR WPI; 2000-533010/48.
XX
PT Synthetic peptides useful for treating cancers and immunosuppressive
PT disorders by disrupting interactions of the SH (Src homology) 2 and SH3
PT motifs of Src family kinase proteins.
XX
PS Claim 3; Page 32; 40pp; English.
XX
CC The present sequence is a synthetic peptide which has a high affinity for
CC the src homology 3 (SH3) domain of protein kinases. Protein kinases are
CC involved in signal transduction pathways, and this peptide can be used to
CC inhibit these, by disrupting protein-protein interactions, in the
CC treatment of cancer, particularly hepatocellular carcinoma, cervical
CC cancer, colon adenocarcinoma and fibrosarcoma, and immune suppression-
CC associated diseases
XX
SQ Sequence 11 AA;

Query Match 32.7%; Score 32; DB 3; Length 11;
Best Local Similarity 50.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 DQPPDVEKPD 10
              ::|| |  ||
Db          2 ERPPPVPNPD 11
```

RESULT 24
AAB21133
ID AAB21133 standard; peptide; 11 AA.
XX
AC AAB21133;
XX
DT 19-JAN-2001 (first entry)
XX
DE Src homology 3 domain binding peptide #10.
XX
KW Src homology domain 3; SH3; protein-protein interaction; cancer;
KW signal transduction inhibition; immune suppression-associated disease.
XX
OS Synthetic.
XX
PN WO200047607-A1.
XX
PD 17-AUG-2000.
XX
PF 12-FEB-2000; 2000WO-KR000107.
XX

PR 12-FEB-1999; 99AU-00008643.
PR 02-JUN-1999; 99KR-00020282.
XX
PA (YOON/) YOON J H.
PA (HANY/) HAN Y T.
XX
PI Yoon JH, Han YT, Lee KY;
XX
DR WPI; 2000-533010/48.
XX
PT Synthetic peptides useful for treating cancers and immunosuppressive
PT disorders by disrupting interactions of the SH (Src homology) 2 and SH3
PT motifs of Src family kinase proteins.
XX
PS Claim 3; Page 35; 40pp; English.
XX
CC The present sequence is a synthetic peptide which has a high affinity for
CC the src homology 3 (SH3) domain of protein kinases. Protein kinases are
CC involved in signal transduction pathways, and this peptide can be used to
CC inhibit these, by disrupting protein-protein interactions, in the
CC treatment of cancer, particularly hepatocellular carcinoma, cervical
CC cancer, colon adenocarcinoma and fibrosarcoma, and immune suppression-
CC associated diseases
XX
SQ Sequence 11 AA;

  Query Match   32.7%; Score 32; DB 3; Length 11;
  Best Local Similarity   50.0%; Pred. No. 4.7e+02;
  Matches   5; Conservative   2; Mismatches   3; Indels   0; Gaps   0;

Qy   1 DQPPDVEKPD 10
              ::|| | ||
Db   2 ERPPPVPNPD 11

RESULT 25
AAU01841
ID AAU01841 standard; peptide; 17 AA.
XX
AC AAU01841;
XX
DT 07-SEP-2001 (first entry)
XX
DE Wheat peptide antagonist for A-gliadin 57-73 QE65 #3.
XX
KW Wheat; A-gliadin; 57-75 QE65; coeliac disease; gluten intolerance;
KW T-cell binding; antagonist; transglutaminase; transgenic plant.
XX
OS Triticum aestivum.
XX
PN WO200125793-A2.
XX
PD 12-APR-2001.
XX
PF 02-OCT-2000; 2000WO-GB003760.
XX
PR 01-OCT-1999; 99GB-00023306.

XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Anderson RP, Hill AVS, Jewell DP;
XX
DR WPI; 2001-300179/31.
XX
PT Diagnosing coeliac disease or susceptibility to the disease in an
PT individual, by detecting in vitro or in vivo T cells which bind
PT immunodominant T cell epitope obtained from naturally occurring homolog
PT of gliadin.
XX
PS Example 11; Page 58; 107pp; English.
XX
CC The sequence represents a gliadin peptide corresponding to A-gliadin 57-
CC 73 which is naturally polymorphic in that region and is antagonistic to A
CC -gliadin 57-73 QE65 interferon gamma ELISpot (not defined) response. The
CC peptides of the invention are used to test mammalian (preferably human)
CC susceptibility to coeliac disease (gluten intolerance). The peptides are
CC contacted with a blood sample and T cell recognition measured, a positive
CC T-cell recognition indicating a susceptibility to coeliac disease. The
CC peptides are useful for inducing tolerance in an individual and
CC antagonists to the peptides are useful for treating or preventing coeliac
CC disease in an individual and for producing an antibody specific to them
CC or a wild-type sequence. A mutant gliadin protein (or its fragment of 15
CC amino acids in length) whose wild-type sequence can be modified by
CC transglutaminase to a sequence that comprises the epitope, but which has
CC been modified in such a way that it does not contain sequence which can
CC be modified by transglutaminase to a sequence that comprise the epitope
CC is useful for decreasing the ability of gliadin protein to cause Coeliac
CC disease. Nucleic acids encoding proteins antagonistic to the T-cell
CC binding of the epitopes are useful for obtaining a transgenic plant cell
CC or seed and for the production of a protein. The resultant crop plant is
CC useful for obtaining a product of a wheat plant, especially grain, which
CC is optionally processed into flour or another grain product. Food
CC comprising the antagonistic protein is useful instead of a wild-type
CC gliadin
XX
SQ Sequence 17 AA;

Query Match 32.7%; Score 32; DB 4; Length 17;
Best Local Similarity 45.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```
Qy          3 PPDVEKPDLQP 13
              ||::  |  ||
Db          7 PPELPYPQTQP 17
```

RESULT 26
AAU01840
ID AAU01840 standard; peptide; 17 AA.
XX
AC AAU01840;
XX
DT 07-SEP-2001 (first entry)
XX

DE Wheat peptide antagonist for A-gliadin 57-73 QE65 #2.
XX
KW Wheat; A-gliadin; 57-75 QE65; coeliac disease; gluten intolerance;
KW T-cell binding; antagonist; transglutaminase; transgenic plant.
XX
OS Triticum aestivum.
XX
PN WO200125793-A2.
XX
PD 12-APR-2001.
XX
PF 02-OCT-2000; 2000WO-GB003760.
XX
PR 01-OCT-1999; 99GB-00023306.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Anderson RP, Hill AVS, Jewell DP;
XX
DR WPI; 2001-300179/31.
XX
PT Diagnosing coeliac disease or susceptibility to the disease in an
PT individual, by detecting in vitro or in vivo T cells which bind
PT immunodominant T cell epitope obtained from naturally occurring homolog
PT of gliadin.
XX
PS Example 11; Page 58; 107pp; English.
XX
CC The sequence represents a gliadin peptide corresponding to A-gliadin 57-
CC 73 which is naturally polymorphic in that region and is antagonistic to A
CC -gliadin 57-73 QE65 interferon gamma ELISpot (not defined) response. The
CC peptides of the invention are used to test mammalian (preferably human)
CC susceptibility to coeliac disease (gluten intolerance). The peptides are
CC contacted with a blood sample and T cell recognition measured, a positive
CC T-cell recognition indicating a susceptibility to coeliac disease. The
CC peptides are useful for inducing tolerance in an individual and
CC antagonists to the peptides are useful for treating or preventing coeliac
CC disease in an individual and for producing an antibody specific to them
CC or a wild-type sequence. A mutant gliadin protein (or its fragment of 15
CC amino acids in length) whose wild-type sequence can be modified by
CC transglutaminase to a sequence that comprises the epitope, but which has
CC been modified in such a way that it does not contain sequence which can
CC be modified by transglutaminase to a sequence that comprise the epitope
CC is useful for decreasing the ability of gliadin protein to cause Coeliac
CC disease. Nucleic acids encoding proteins antagonistic to the T-cell
CC binding of the epitopes are useful for obtaining a transgenic plant cell
CC or seed and for the production of a protein. The resultant crop plant is
CC useful for obtaining a product of a wheat plant, especially grain, which
CC is optionally processed into flour or another grain product. Food
CC comprising the antagonistic protein is useful instead of a wild-type
CC gliadin
XX
SQ Sequence 17 AA;

Query Match 32.7%; Score 32; DB 4; Length 17;
Best Local Similarity 45.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```
Qy          3 PPDVEKPDLQP 13
              ||::  |  ||
Db          7 PPELPYPQTQP 17


RESULT 27
AAW38909
ID   AAW38909 standard; peptide; 18 AA.
XX
AC   AAW38909;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Peptide resembling an SH3 domain binding peptide SEQ ID NO:305.
XX
KW   Cortactin; SH3 domain; binding peptide; Src homology region 3;
KW   tyrosine kinase; immune response; lymphokine; interleukin 1; Nck; Abl;
KW   PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
OS   Synthetic.
XX
PN   WO9730074-A1.
XX
PD   21-AUG-1997.
XX
PF   14-FEB-1997;   97WO-US002298.
XX
PR   16-FEB-1996;   96US-00602999.
XX
PA   (CYTO-) CYTOGEN CORP.
PA   (UYNC-) UNIV NORTH CAROLINA.
XX
PI   Sparks AB,  Kay BK,  Thorn JM,  Quilliam LA,  Der CJ,  Fowlkes DM;
PI   Rider JE;
XX
DR   WPI; 1997-424972/39.
XX
PT   Src homology region 3 binding peptide - used to activate Src tyrosine
PT   kinase(s) and to stimulate immune response by increasing production of
PT   certain lymphokine(s), e.g. interleukin-1.
XX
PS   Claim 22; Page 90; 131pp; English.
XX
CC   The present sequence represents a peptide which resembles a Src homology
CC   region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
CC   (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
CC   bind the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain
CC   of Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which
CC   bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain
CC   of p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
CC   (h) peptides which bind the SH3 domain of Yes; and (i) peptides which
CC   bind the amino-terminal SH3 domain of Grb2. The purified binding peptides
CC   can be used in the method to identify inhibitors of their binding to
CC   their respective SH3 domains, which could be used to modulate the
CC   pharmacological activity of proteins or polypeptide containing the SH3
CC   domain. The peptides can also be used to activate Src or Src-related
```

CC protein tyrosine kinases, to stimulate the immune response by increasing
CC the production of certain lymphokines, e.g. tumour necrosis factor-alpha
CC and interleukin-1, or to deliver a conjugated molecule to certain
CC cellular compartments containing Src or Src related proteins
XX
SQ Sequence 18 AA;

Query Match 32.7%; Score 32; DB 2; Length 18;
Best Local Similarity 43.8%; Pred. No. 7.8e+02;
Matches 7; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```
Qy          2 QPPDVEKPDLQPFQVQ 17
              |||    |  ||   |
Db          3 QPPYFPPPPYQPIYPQ 18
```

RESULT 28
AAG97089
ID AAG97089 standard; peptide; 10 AA.
XX
AC AAG97089;
XX
DT 18-SEP-2001 (first entry)
XX
DE Human complementary peptide, SEQ ID NO: 3283.
XX
KW Human; complementary peptide; ligand; drug discovery; drug design.
XX
OS Homo sapiens.
XX
PN WO200142277-A2.
XX
PD 14-JUN-2001.
XX
PF 13-DEC-2000; 2000WO-GB004776.
XX
PR 13-DEC-1999; 99GB-00029464.
XX
PA (PROT-) PROTEOM LTD.
XX
PI Roberts GW, Heal JR;
XX
DR WPI; 2001-408419/43.
XX
PT A set of peptide ligands consisting of specific complementary peptides to
PT proteins encoded by genes of the human genome, useful in an assay for
PT screening and identifying of one or more novel peptides which are drug
PT candidates or pro-drugs.
XX
PS Example 4; Page 515; 646pp; English.
XX
CC The invention relates to a set of complementary peptide ligands generated
CC from the human genome. The complementary peptides interact with their
CC relevant target proteins encoded in the human genome. They can be used as
CC reagents in drug discovery and as lead ligands to facilitate drug design
CC and development. The present sequence is a complementary peptide provided
CC in the specification

XX
SQ Sequence 10 AA;

  Query Match 31.6%; Score 31; DB 4; Length 10;
  Best Local Similarity 71.4%; Pred. No. 5.9e+02;
  Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPDVEKP 9
      || |:||
Db 3 PPTVQKP 9

RESULT 29
AAW17451
ID AAW17451 standard; peptide; 11 AA.
XX
AC AAW17451;
XX
DT 17-JUN-1997 (first entry)
XX
DE Consensus antibacterial peptide from Podisus maculiventris.
XX
KW Podisus maculiventris; proline-rich; pathogenic; bacteria; bug;
KW Gram negative; plant treatment.
XX
OS Podisus maculiventris.
XX
FH Key Location/Qualifiers
FT Misc-difference 11
FT /note= "X= a peptide residue comprising at least one
FT tripeptide Pro-Arg-Pro motif"
XX
PN FR2732345-A1.
XX
PD 04-OCT-1996.
XX
PF 03-APR-1995; 95FR-00004130.
XX
PR 03-APR-1995; 95FR-00004130.
XX
PA (RHON) RHONE POULENC AGROCHIMIE.
XX
PI Bulet P, Hoffman J, Hetru C, Tchernych S;
XX
DR WPI; 1996-457711/46.
XX
PT Proline-rich antibacterial peptide(s) from Podisus maculiventris - esp.
PT useful to protect plants against pathogenic bacteria, also for
PT antibacterial therapy of animals.
XX
PS Claim 1; Page 14; 16pp; English.
XX
CC AAW17451 is a generic sequence of an antibacterial peptide from the bug
CC Podisus maculoventris. The proline-rich peptide has antibacterial
CC activity against gram negative bacteria. It is useful for protecting
CC plants against pathogenic bacteria, but could also be used for
CC antibacterial therapy of animals, including humans. For specific examples

CC see AAW09375-W09378
XX
SQ Sequence 11 AA;

Query Match 31.6%; Score 31; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 6.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          6 VEKPDLQP 13
              |:||| :|
Db          1 VDKPDYRP 8
```

RESULT 30
ABP61522
ID ABP61522 standard; peptide; 11 AA.
XX
AC ABP61522;
XX
DT 02-OCT-2002 (first entry)
XX
DE Human KRPI tryptic digest peptide #34.
XX
KW Human; tryptic digest peptide; KRPI; kidney response; KR;
KW nephrotropic kidney response-associated protein isoform; gene therapy;
KW antisense therapy; kidney function; tubular nephritis; renal failure;
KW nephron cell metabolic pathway modulation; glomerular necrosis;
KW papillary necrosis.
XX
OS Homo sapiens.
XX
PN WO200254081-A2.
XX
PD 11-JUL-2002.
XX
PF 24-DEC-2001; 2001WO-GB005777.
XX
PR 29-DEC-2000; 2000US-0260392P.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Holt GD, Kelly MD, Kennedy SJ, Moyses C;
XX
DR WPI; 2002-583637/62.
XX
PT Screening, diagnosis or prognosis of kidney response in subject, by
PT detecting kidney response-associated features or kidney response-
PT associated protein isoforms in body fluid or tissue from subject.
XX
PS Disclosure; Page 39; 168pp; English.
XX
CC The invention relates to a novel method for the screening, diagnosis or
CC prognosis of kidney response (KR). The method of the invention has
CC nephrotropic activity, and may have a use in gene therapy or antisense
CC therapy. The method is useful for the screening, diagnosis or prognosis
CC of KR in a subject, for determining the stage or severity of KR in a
CC subject, for identifying a subject at risk of developing KR, or for

CC monitoring the effect of therapy administered to a subject with KR. An
CC alternative method of the invention is useful for screening agents that
CC interact with one or more of the kidney response-associated protein
CC isoforms (KRPIs). The kidney response includes alterations in kidney
CC function, any phase of nephron cell metabolic pathway modulation,
CC glomerular/proximal tubular nephritis, glomerular/papillary necrosis,
CC acute and chronic renal failure, and end stage renal disease. The
CC sequences shown in ABP61514-ABP61787 represent tryptic digest peptides of
CC the KRPIs of the invention
XX
SQ Sequence 11 AA;

Query Match 31.6%; Score 31; DB 5; Length 11;
Best Local Similarity 55.6%; Pred. No. 6.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy          7 EKPDLQPFQ 15
              : |:| |||
Db          2 DNPNLPPFQ 10
```

RESULT 31
AAW45819
ID AAW45819 standard; peptide; 15 AA.
XX
AC AAW45819;
XX
DT 25-JUN-1998 (first entry)
XX
DE Peptide recognised by anti HSV-2 glycoprotein G (gG) antibody E5.
XX
KW Glycoprotein G; herpes simplex virus type 2; HSV-2 gG; anti-gG2;
KW HSV-2 infection; vaccine; diagnosis.
XX
OS Synthetic.
XX
PN WO9803544-A1.
XX
PD 29-JAN-1998.
XX
PF 24-JUL-1997; 97WO-GB002003.
XX
PR 24-JUL-1996; 96GB-00015533.
XX
PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
PI Grabowska AM, Irving WL, Laing P;
XX
DR WPI; 1998-120696/11.
XX
PT Polypeptide antigen of Herpes simplex virus 2 glycoprotein G - used to
PT create antibodies for treating HSV-2 infection.
XX
PS Disclosure; Page 36; 63pp; English.
XX
CC This sequence is shown in the specification. The invention relates to a
CC novel polypeptide which comprises 3-20 amino acids, or a peptidomimetic

CC analogue of it where the analogue is at least partly non-peptide in
CC nature and the analogue has a length equivalent to that determined by 3-
CC 20 amino acid residues, which is a sequence not naturally occurring in
CC the native sequence of the Herpes simplex virus glycoprotein G (HSV-2 gG
CC protein), and has one of the following sequences: (X)n- alpha - beta -
CC gamma -(Y)m (I); or (X)n- delta - epsilon - theta -(Y)m (II); n = 0 or an
CC integer; m = 0 or an integer; n+m at most 17; alpha is E or may be
CC substituted in order of preference by D greater than T greater than S
CC greater than Q greater than N; beta is H; gamma is R or may be
CC substituted in order of preference by R greater than A or L greater than
CC T or P; epsilon is P; theta is L or may be substituted in order of
CC preference by B or Y; and X or Y are positively charged, negatively
CC charged or neutral amino acids or peptidomimetics thereof. The
CC polypeptide can be used in vaccine compositions, which can be used to
CC prevent HSV-2 infection. It can also be used to test for the presence of
CC type-specific HSV-2 gG2 antibodies in a fluid. This test can be used to
CC diagnose HSV-2 infection
XX
SQ Sequence 15 AA;

Query Match 31.6%; Score 31; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 9e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 DQPPDVEKPD 10
              | || :  ||
Db          5 DPPPPLHAPD 14
```

RESULT 32
AAW45614
ID AAW45614 standard; peptide; 15 AA.
XX
AC AAW45614;
XX
DT 24-JUN-1998 (first entry)
XX
DE Peptide recognised by anti HSV-2 glycoprotein G (gG) antibody E5.
XX
KW Antigenic peptide; herpes simplex virus type 2; HSV-2; glycoprotein-G;
KW gG; vaccine; HSV-2 infection; diagnose.
XX
OS Synthetic.
XX
PN WO9803543-A1.
XX
PD 29-JAN-1998.
XX
PF 24-JUL-1997; 97WO-GB001990.
XX
PR 24-JUL-1996; 96GB-00015533.
XX
PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
PI Grabowska AM, Irving WL, Laing P;
XX
DR WPI; 1998-120695/11.

XX
PT Polypeptide antigen of Herpes simplex virus 2 glycoprotein G - used to
PT create antibodies for treating HSV-2 infection.
XX
PS Disclosure; Page 32; 61pp; English.
XX
CC Peptides AAW45608-15 represent antigenic peptides that are recognised by
CC antibodies against the herpes simplex virus type 2 (HSV-2) glycoprotein-G
CC (gG). They were isolated from a library of phage containing random 15-mer
CC peptide inserts that was screened with the murine monoclonal antibody
CC O1B90.E5 (E5). The peptides are not recognised by anti-gG2 negative sera
CC from patients with HSV-1 infection. The specification describes a
CC filamentous bacteriophage including in a portion of its major coat
CC protein sub-units multiple display of the peptide (or its analogues). The
CC peptides and the filamentous bacteriophage can be used in vaccine
CC compositions, which can be used to prevent HSV-2 infection. The peptides
CC and antibodies against them can be used to test for the presence of type-
CC specific HSV-2 gG2 antibodies in a fluid. This test can be used to
CC diagnose HSV-2 infection
XX
SQ Sequence 15 AA;

Query Match 31.6%; Score 31; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 9e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 DQPPDVEKPD 10
              | || :  ||
Db          5 DPPPPLHAPD 14
```

RESULT 33
AAW09376
ID AAW09376 standard; peptide; 16 AA.
XX
AC AAW09376;
XX
DT 17-JUN-1997 (first entry)
XX
DE Proline-rich antibacterial peptide from Podisus maculiventris.
XX
KW Podisus maculiventris; proline-rich; pathogenic; bacteria; bug;
KW Gram negative; plant treatment.
XX
OS Podisus maculiventris.
XX
PN FR2732345-A1.
XX
PD 04-OCT-1996.
XX
PF 03-APR-1995; 95FR-00004130.
XX
PR 03-APR-1995; 95FR-00004130.
XX
PA (RHON) RHONE POULENC AGROCHIMIE.
XX
PI Bulet P, Hoffman J, Hetru C, Tchernych S;

XX
DR WPI; 1996-457711/46.
XX
PT Proline-rich antibacterial peptide(s) from Podisus maculiventris - esp.
PT useful to protect plants against pathogenic bacteria, also for
PT antibacterial therapy of animals.
XX
PS Claim 2; Page 14; 16pp; English.
XX
CC AAW09375-W09378 are specific examples of antibacterial peptides from the
CC bug Podisus maculoventris. The proline-rich peptides have antibacterial
CC activity against gram negative bacteria. They are useful for protecting
CC plants against pathogenic bacteria, but could also be used for
CC antibacterial therapy of animals, including humans. A generic peptide
CC having the sequence VDKPDYRPRPX is also given in the specification, where
CC X is a peptide comprising at least one PRP motif (see AAW17451)
XX
SQ Sequence 16 AA;

Query Match 31.6%; Score 31; DB 2; Length 16;
Best Local Similarity 62.5%; Pred. No. 9.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          6 VEKPDLQP 13
              |:||| :|
Db          1 VDKPDYRP 8
```

RESULT 34
AAW09377
ID AAW09377 standard; peptide; 16 AA.
XX
AC AAW09377;
XX
DT 17-JUN-1997 (first entry)
XX
DE Proline-rich antibacterial peptide from Podisus maculiventris.
XX
KW Podisus maculiventris; proline-rich; pathogenic; bacteria; bug;
KW Gram negative; plant treatment.
XX
OS Podisus maculiventris.
XX
PN FR2732345-A1.
XX
PD 04-OCT-1996.
XX
PF 03-APR-1995; 95FR-00004130.
XX
PR 03-APR-1995; 95FR-00004130.
XX
PA (RHON) RHONE POULENC AGROCHIMIE.
XX
PI Bulet P, Hoffman J, Hetru C, Tchernych S;
XX
DR WPI; 1996-457711/46.
XX

PT Proline-rich antibacterial peptide(s) from Podisus maculiventris - esp.
PT useful to protect plants against pathogenic bacteria, also for
PT antibacterial therapy of animals.
XX
PS Claim 2; Page 14; 16pp; English.
XX
CC AAW09375-W09378 are specific examples of antibacterial peptides from the
CC bug Podisus maculoventris. The proline-rich peptides have antibacterial
CC activity against gram negative bacteria. They are useful for protecting
CC plants against pathogenic bacteria, but could also be used for
CC antibacterial therapy of animals, including humans. A generic peptide
CC having the sequence VDKPDYRPRPX is also given in the specification, where
CC X is a peptide comprising at least one PRP motif (see AAW17451)
XX
SQ Sequence 16 AA;

Query Match 31.6%; Score 31; DB 2; Length 16;
Best Local Similarity 62.5%; Pred. No. 9.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          6 VEKPDLQP 13
              |:||| :|
Db          1 VDKPDYRP 8
```

RESULT 35
AAW12220
ID AAW12220 standard; peptide; 17 AA.
XX
AC AAW12220;
XX
DT 25-MAR-2003 (revised)
DT 25-MAR-1997 (first entry)
XX
DE Human acetylcholine receptor alpha chain amino acid 158-174.
XX
KW Tolerogenic conjugate; derivatisation; polymer; polyethylene glycol;
KW polyvinyl alcohol; immunotherapy; myasthenia gravis; autoimmune disease;
KW Grave's disease; allergy; antibody response.
XX
OS Synthetic.
XX
PN US5578496-A.
XX
PD 26-NOV-1996.
XX
PF 05-OCT-1994; 94US-00318200.
XX
PR 19-DEC-1991; 91US-00811050.
PR 20-OCT-1992; 92US-00965670.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Ashizawa T, Atassi MZ;
XX
DR WPI; 1997-020422/02.
XX

PT Diagnosing myasthenia gravis by detecting auto-antibodies to
PT acetyl:choline receptor - using set of peptide(s) derived from the
PT extracellular domain of the receptor, also therapeutic tolerogenic
PT peptide conjugates.
XX
PS Example 5; Col 41-42; 40pp; English.
XX
CC The peptides AAW12206-24 are derived from the human acetylcholine
CC receptor alpha-chain. This peptide corresponds to amino acids 158-174 of
CC the alpha-chain. The peptides are pref. derived from the extracellular
CC domain of the acetylcholine receptor. They are used in a method of
CC diagnosing an autoimmune disease, esp. myasthenia gravis, by recognising
CC autoantibodies associated with this disease. The peptides can also be
CC used to generate tolerogenic conjugates by derivatising the N-terminal
CC residue with a tolerogenic polymer, esp. monomethoxy-polyethylene glycol
CC or polyvinyl alcohol. The conjugates are esp. used for immunotherapy of
CC myasthenia gravis or other autoimmune disease such as Grave's disease, or
CC allergies, by suppressing antibody responses. (Updated on 25-MAR-2003 to
CC correct PF field.)
XX
SQ Sequence 17 AA;

Query Match 31.6%; Score 31; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. No. 1e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```
Qy          4 PDVEKPDLQPF 14
              |: ::|||  |
Db          3 PESDQPDLSNF 13
```

RESULT 36
AAW09378
ID AAW09378 standard; peptide; 18 AA.
XX
AC AAW09378;
XX
DT 17-JUN-1997 (first entry)
XX
DE Proline-rich antibacterial peptide from Podisus maculiventris.
XX
KW Podisus maculiventris; proline-rich; pathogenic; bacteria; bug;
KW Gram negative; plant treatment.
XX
OS Podisus maculiventris.
XX
PN FR2732345-A1.
XX
PD 04-OCT-1996.
XX
PF 03-APR-1995; 95FR-00004130.
XX
PR 03-APR-1995; 95FR-00004130.
XX
PA (RHON) RHONE POULENC AGROCHIMIE.
XX
PI Bulet P, Hoffman J, Hetru C, Tchernych S;

XX
DR WPI; 1996-457711/46.
XX
PT Proline-rich antibacterial peptide(s) from Podisus maculiventris - esp.
PT useful to protect plants against pathogenic bacteria, also for
PT antibacterial therapy of animals.
XX
PS Claim 2; Page 14; 16pp; English.
XX
CC AAW09375-W09378 are specific examples of antibacterial peptides from the
CC bug Podisus maculoventris. The proline-rich peptides have antibacterial
CC activity against gram negative bacteria. They are useful for protecting
CC plants against pathogenic bacteria, but could also be used for
CC antibacterial therapy of animals, including humans. A generic peptide
CC having the sequence VDKPDYRPRPX is also given in the specification, where
CC X is a peptide comprising at least one PRP motif (see AAW17451)
XX
SQ Sequence 18 AA;

Query Match 31.6%; Score 31; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          6 VEKPDLQP 13
              |:||| :|
Db          1 VDKPDYRP 8
```

RESULT 37
AAR44563
ID AAR44563 standard; protein; 11 AA.
XX
AC AAR44563;
XX
DT 25-MAR-2003 (revised)
DT 26-MAY-1994 (first entry)
XX
DE Encoded by human Ews exon 10/Hum-Fli-1 exon 8 fusion.
XX
KW chromosomal translocation; chimeric; chimaeric; Ewing sarcoma; Ews gene;
KW malignant melanoma; hum-fli-1;
KW primitive peripheral neuroectodermal tumour; human chromosome 11;
KW human chromosome 22.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1. .5
FT /note= "encoded by 3'-end of Ews exon 10"
FT Region 6. .11
FT /note= "encoded by 5'-end of Hum-Fli-1 exon 8"
XX
PN WO9323549-A2.
XX
PD 25-NOV-1993.
XX
PF 19-MAY-1993; 93WO-FR000494.

XX
PR 20-MAY-1992; 92FR-00006123.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Aurias A, Delattre O, Desmaze C, Melot T, Peter M, Plougastel B;
PI Thomas G, Zucman J;
XX
DR WPI; 1993-386580/48.
DR N-PSDB; AAQ50676.
XX
PT New nucleic acid of EWS gene and its hybrid(s) - contg. gene sequence
PT involved in chromosomal trans-location, also derived mRNA, probes, fusion
PT proteins etc., for diagnosis and treatment of Ewing sarcoma and melanoma.
XX
PS Disclosure; Fig 14; 123pp; French.
XX
CC The intron-exon junctions of the human Ews gene and the Hum-Fli-1 gene
CC have been sequenced (see AAQ50646 and AAQ50662, respectively). The
CC different fusion products which could be formed by fusing exons from the
CC two genes, as happens after specific chromosomal translocations, can be
CC predicted. See AAR44558-R44565 for the amino acid sequences resulting
CC from the different fusion events. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 11 AA;

  Query Match   31.1%; Score 30.5; DB 2; Length 11;
  Best Local Similarity   46.2%; Pred. No. 7.7e+02;
  Matches   6; Conservative   3; Mismatches   1; Indels   3; Gaps   1;

Qy   4 PDVEKPDLQPFQV 16
              ||: || |:|:
Db   1 PDL---DLDPYQI 10

RESULT 38
ABP55802
ID ABP55802 standard; peptide; 9 AA.
XX
AC ABP55802;
XX
DT 25-FEB-2003 (first entry)
XX
DE B15 class I sHLA molecule ligand related peptide #96.
XX
KW HLA ligand; human leukocyte antigen; predictive algorithm; database;
KW MHC ligand; major histocompatibility complex; viral; bacterial; tumour.
XX
OS Synthetic.
XX
PN WO200269198-A2.
XX
PD 06-SEP-2002.
XX
PF 21-FEB-2002; 2002WO-US005298.
XX

PR 21-FEB-2001; 2001US-0270357P.
PR 10-OCT-2001; 2001US-00974366.
PR 18-DEC-2001; 2001US-00022066.
XX
PA (HILD/) HILDEBRAND W H.
PA (PRIL/) PRILLIMAN K R.
PA (HICK/) HICKMAN H D.
XX
PI Hildebrand WH, Prilliman KR, Hickman HD;
XX
DR WPI; 2002-732755/79.
XX
PT Human leukocyte antigen ligand database assembled by producing HLA having
PT loaded ligands, isolating and sequencing loaded ligands to obtain HLA
PT ligand data and populating database in computer system with ligand data.
XX
PS Disclosure; Fig 5; 118pp; English.
XX
CC The present invention describes a human leukocyte antigen (HLA) (e.g.
CC soluble HLA) ligand database assembled by a process which involves
CC providing a computer system capable of storing HLA data as a database,
CC producing HLA having ligands loaded on it, isolating the loaded ligands
CC from HLA, sequencing the loaded ligands to obtain HLA ligand data, and
CC populating the database with HLA ligand data. Also described: (1)
CC accessing HLA (e.g. sHLA) data stored in a database; and (2) a computer
CC system for HLA (e.g. sHLA) ligand database. The database is populated
CC with HLA ligand sequences, motifs, extended motifs, submotifs, ligands
CC unique to infected cells, tumour specific ligands, as well as a
CC collection of current and future developed HLA ligand sequences. The
CC database which contains endogenously bound and loaded ligands facilitates
CC searching of viral, bacterial, tumour or human protein sequences for
CC ligands likely to bind a particular HLA class I or class II protein. The
CC database allows the user to screen an unknown peptide sequence for
CC potential matches with sHLA ligand discrete sequences or sHLA ligand
CC motifs of sequences. Due to the completeness and concentration of sHLA
CC obtained to date, better sequencing data of numerous endogenously loaded
CC HLA ligands is found in the sHLA ligand database, and by comparison of
CC such ligands to each other and to the genomic sequence, better motifs are
CC also found in the sHLA ligand database. ABP55692 to ABP55912 represent
CC amino acid sequences used in the exemplification of the present invention
XX
SQ Sequence 9 AA;

  Query Match   30.6%; Score 30; DB 5; Length 9;
  Best Local Similarity   57.1%; Pred. No. 1.4e+06;
  Matches   4; Conservative   2; Mismatches   1; Indels   0; Gaps   0;

Qy   1 DQPPDVE 7
              | |||::
Db   2 DPPPDMZ 8

RESULT 39
ABG96846
ID ABG96846 standard; peptide; 9 AA.
XX
AC ABG96846;

XX

DT 16-DEC-2002 (first entry)

XX

DE Human leukocyte antigen (HLA) B15 ligand #171.

XX

KW Soluble human leukocyte antigen; HLA; sHLA; cell pharm;
KW multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response;
KW viral infection; cancer; autoimmune disease; vaccine development; MHC;
KW major histocompatibility complex; diagnostic development;
KW HLA class I polymorphism; HLA-B15 allotype; ligand.

XX

OS Homo sapiens.

XX

PN WO200262846-A2.

XX

PD 15-AUG-2002.

XX

PF 18-DEC-2001; 2001WO-US049744.

XX

PR 18-DEC-2000; 2000US-0256409P.
PR 18-DEC-2000; 2000US-0256410P.
PR 10-OCT-2001; 2001US-00974366.

XX

PA (HILD/) HILDEBRAND W H.
PA (PRIL/) PRILLIMAN K R.

XX

PI Hildebrand WH, Prilliman KR;

XX

DR WPI; 2002-698563/75.

XX

PT Producing soluble human leukocyte antigen (HLA) in cell pharm useful for
PT studies of peptide loading for characterizing human immune responses
PT involves using HLA allelic cDNA or genomic DNA as starting material.

XX

PS Disclosure; Page 178; 300pp; English.

XX

CC The invention describes a method of producing soluble human leukocyte
CC antigen (HLA) molecules (sHLA) in cell pharm involving amplifying HLA
CC allelic DNA by PCR using a locus specific primer to produce truncated a
CC PCR product (PI), inserting P1 into mammalian expression vector;
CC electroporating the plasmid into a host cell; inoculating the cell pharm
CC with the host cell such that cell pharm produces sHLA. A multimeric HLA
CC complex (I) is useful for testing functionality of peptide ligands bound
CC by at least two soluble HLA molecules. (I) can be tested for its ability
CC to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune
CC responses in humans. (I) is useful for studying T cell responses to
CC pathological conditions such as viral infections and cancer, and for
CC modulating the human immune system to induce tolerance in autoimmune
CC diseases. The individual secreted major histocompatibility complex (MHC)
CC molecules produced are useful for studies of peptide loading (i.e., in
CC vaccine development) and to the development of diagnostics. With the
CC secreted MHC molecules, naturally loaded peptides can be eluted from the
CC MHC molecule and characterised. The secreted MHC molecules allow the
CC assessment of structural and functional impact of HLA class I
CC polymorphism. The molecules are also useful to generate ligands and hence
CC ligand maps from the peptide pools extracted from series of distinct yet
CC related class I HLA-B15 allotypes; compare the different ligand maps to

CC identify potentially shared elements; and characterise the elements
CC identified to positively or negatively validate the occurrence of
CC overlapping ligands. The truncated version of (MHC) can be produced in
CC mammalian or insect/bacterial cells such that milligram or greater
CC quantities of an individual class I or class II molecule can be obtained.
CC This sequence represents a HLA (human leukocyte antigen) peptide ligand
XX
SQ Sequence 9 AA;

Query Match 30.6%; Score 30; DB 5; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 DQPPDVE 7
              | |||:: 
Db          2 DPPPDMZ 8
```

RESULT 40
ABG96954
ID ABG96954 standard; peptide; 9 AA.
XX
AC ABG96954;
XX
DT 16-DEC-2002 (first entry)
XX
DE Human leukocyte antigen (HLA) B15 ligand #282.
XX
KW Soluble human leukocyte antigen; HLA; sHLA; cell pharm;
KW multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response;
KW viral infection; cancer; autoimmune disease; vaccine development; MHC;
KW major histocompatibility complex; diagnostic development;
KW HLA class I polymorphism; HLA-B15 allotype; ligand.
XX
OS Homo sapiens.
XX
PN WO200262846-A2.
XX
PD 15-AUG-2002.
XX
PF 18-DEC-2001; 2001WO-US049744.
XX
PR 18-DEC-2000; 2000US-0256409P.
PR 18-DEC-2000; 2000US-0256410P.
PR 10-OCT-2001; 2001US-00974366.
XX
PA (HILD/) HILDEBRAND W H.
PA (PRIL/) PRILLIMAN K R.
XX
PI Hildebrand WH, Prilliman KR;
XX
DR WPI; 2002-698563/75.
XX
PT Producing soluble human leukocyte antigen (HLA) in cell pharm useful for
PT studies of peptide loading for characterizing human immune responses
PT involves using HLA allelic cDNA or genomic DNA as starting material.
XX

PS Disclosure; Page 181; 300pp; English.
XX
CC The invention describes a method of producing soluble human leukocyte
CC antigen (HLA) molecules (sHLA) in cell pharm involving amplifying HLA
CC allelic DNA by PCR using a locus specific primer to produce truncated a
CC PCR product (PI), inserting P1 into mammalian expression vector;
CC electroporating the plasmid into a host cell; inoculating the cell pharm
CC with the host cell such that cell pharm produces sHLA. A multimeric HLA
CC complex (I) is useful for testing functionality of peptide ligands bound
CC by at least two soluble HLA molecules. (I) can be tested for its ability
CC to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune
CC responses in humans. (I) is useful for studying T cell responses to
CC pathological conditions such as viral infections and cancer, and for
CC modulating the human immune system to induce tolerance in autoimmune
CC diseases. The individual secreted major histocompatibility complex (MHC)
CC molecules produced are useful for studies of peptide loading (i.e., in
CC vaccine development) and to the development of diagnostics. With the
CC secreted MHC molecules, naturally loaded peptides can be eluted from the
CC MHC molecule and characterised. The secreted MHC molecules allow the
CC assessment of structural and functional impact of HLA class I
CC polymorphism. The molecules are also useful to generate ligands and hence
CC ligand maps from the peptide pools extracted from series of distinct yet
CC related class I HLA-B15 allotypes; compare the different ligand maps to
CC identify potentially shared elements; and characterise the elements
CC identified to positively or negatively validate the occurrence of
CC overlapping ligands. The truncated version of (MHC) can be produced in
CC mammalian or insect/bacterial cells such that milligram or greater
CC quantities of an individual class I or class II molecule can be obtained.
CC This sequence represents a HLA (human leukocyte antigen) peptide ligand
XX
SQ Sequence 9 AA;

Query Match 30.6%; Score 30; DB 5; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 DQPPDVE 7
              | |||::
Db          2 DPPPDMZ 8
```

RESULT 41
ABG96698
ID ABG96698 standard; peptide; 9 AA.
XX
AC ABG96698;
XX
DT 16-DEC-2002 (first entry)
XX
DE Human leukocyte antigen (HLA) B15 ligand #121.
XX
KW Soluble human leukocyte antigen; HLA; sHLA; cell pharm;
KW multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response;
KW viral infection; cancer; autoimmune disease; vaccine development; MHC;
KW major histocompatibility complex; diagnostic development;
KW HLA class I polymorphism; HLA-B15 allotype; ligand.
XX

OS Homo sapiens.
XX
PN WO200262846-A2.
XX
PD 15-AUG-2002.
XX
PF 18-DEC-2001; 2001WO-US049744.
XX
PR 18-DEC-2000; 2000US-0256409P.
PR 18-DEC-2000; 2000US-0256410P.
PR 10-OCT-2001; 2001US-00974366.
XX
PA (HILD/) HILDEBRAND W H.
PA (PRIL/) PRILLIMAN K R.
XX
PI Hildebrand WH, Prilliman KR;
XX
DR WPI; 2002-698563/75.
XX
PT Producing soluble human leukocyte antigen (HLA) in cell pharm useful for
PT studies of peptide loading for characterizing human immune responses
PT involves using HLA allelic cDNA or genomic DNA as starting material.
XX
PS Disclosure; Fig 26; 300pp; English.
XX
CC The invention describes a method of producing soluble human leukocyte
CC antigen (HLA) molecules (sHLA) in cell pharm involving amplifying HLA
CC allelic DNA by PCR using a locus specific primer to produce truncated a
CC PCR product (PI), inserting P1 into mammalian expression vector;
CC electroporating the plasmid into a host cell; inoculating the cell pharm
CC with the host cell such that cell pharm produces sHLA. A multimeric HLA
CC complex (I) is useful for testing functionality of peptide ligands bound
CC by at least two soluble HLA molecules. (I) can be tested for its ability
CC to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune
CC responses in humans. (I) is useful for studying T cell responses to
CC pathological conditions such as viral infections and cancer, and for
CC modulating the human immune system to induce tolerance in autoimmune
CC diseases. The individual secreted major histocompatibility complex (MHC)
CC molecules produced are useful for studies of peptide loading (i.e., in
CC vaccine development) and to the development of diagnostics. With the
CC secreted MHC molecules, naturally loaded peptides can be eluted from the
CC MHC molecule and characterised. The secreted MHC molecules allow the
CC assessment of structural and functional impact of HLA class I
CC polymorphism. The molecules are also useful to generate ligands and hence
CC ligand maps from the peptide pools extracted from series of distinct yet
CC related class I HLA-B15 allotypes; compare the different ligand maps to
CC identify potentially shared elements; and characterise the elements
CC identified to positively or negatively validate the occurrence of
CC overlapping ligands. The truncated version of (MHC) can be produced in
CC mammalian or insect/bacterial cells such that milligram or greater
CC quantities of an individual class I or class II molecule can be obtained.
CC This sequence represents a HLA (human leukocyte antigen) peptide ligand
XX
SQ Sequence 9 AA;

Query Match 30.6%; Score 30; DB 5; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 DQPPDVE 7
              | |||:: 
Db          2 DPPPDMZ 8
```

RESULT 42
ADC35017
ID ADC35017 standard; peptide; 11 AA.
XX
AC ADC35017;
XX
DT 18-DEC-2003 (first entry)
XX
DE Rho-like protein C-terminal peptide #14.
XX
KW protein transduction domain; PTD; cell-penetrating capacity; C-terminus;
KW Ras-like GTPase; Ras-like GTPase inhibition;
KW leukaemic cell migration inhibition; leukaemia; Rho-like protein.
XX
OS Unidentified.
XX
PN WO2003042239-A1.
XX
PD 22-MAY-2003.
XX
PF 11-NOV-2002; 2002WO-NL000722.
XX
PR 12-NOV-2001; 2001EP-00204305.
XX
PA (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING.
XX
PI Ten Klooster JP, Van Hennik PB, Voermans C, Hordijk PL;
XX
DR WPI; 2003-568944/53.
XX
PT New protein transduction domain peptides having cell-penetrating
PT capacity, are useful for inhibiting cellular functions mediated by the
PT Ras-like GTPase in eukaryotic cells, and for inhibiting leukemic cell
PT migration.
XX
PS Disclosure; Page 14; 46pp; English.
XX
CC The invention comprises amino acid sequences corresponding to a protein
CC transduction domain (PTD) which has a cell-penetrating capacity and an
CC amino acid sequence corresponding to a variable part of the C-terminus of
CC a Ras-like GTPase having Ras-like GTPase signalling capacity. The
CC peptides of the invention are useful for inhibiting cellular functions
CC mediated by the Ras-like GTPase in eukaryotic cells - particularly
CC mammalian cells, and for inhibiting leukaemic cell migration. The present
CC amino acid sequence represents a C-terminal sequence from a Rho-like
CC protein.
XX
SQ Sequence 11 AA;

Query Match 30.6%; Score 30; DB 7; Length 11;

Best Local Similarity 71.4%; Pred. No. 9.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 PPDVEKP 9
              || |:||
Db          2 PPPVKKP 8
```

RESULT 43
ABB97741
ID ABB97741 standard; peptide; 13 AA.
XX
AC ABB97741;
XX
DT 11-JUL-2002 (first entry)
XX
DE Human procathepsin W epitope peptide #121.
XX
KW Human; procathepsin W; cathepsin W; monoclonal antibody; epitope.
XX
OS Homo sapiens.
XX
PN WO200226831-A1.
XX
PD 04-APR-2002.
XX
PF 09-JUL-2001; 2001WO-EP007877.
XX
PR 29-SEP-2000; 2000DE-01048727.
XX
PA (LABS-) LABSOFT DIAGNOSTICS AG.
XX
PI Weber E;
XX
DR WPI; 2002-330095/36.
XX
PT New hybridoma cell lines that produces antibodies specific for human
PT cathepsin W, useful e.g. for diagnosis, therapy and drug targeting.
XX
PS Disclosure; Fig 1; 23pp; German.
XX
CC The present invention relates to hybridoma cell lines that produce
CC monoclonal antibodies directed against a defined epitope of human
CC (pro)cathepsin W, which are produced by fusing myeloma cells with spleen
CC cells from an animal that has been immunised with recombinant
CC procathepsin W. The antibodies produced are useful for analysis,
CC diagnosis (detection of human (pro)cathepsin W), purification of
CC (pro)cathepsin W (also for clarifying processing of the precursor and
CC functional significance of the mature protein), for drug targeting and
CC for therapeutic use. The present sequence is an epitope of human
CC procathepsin W
XX
SQ Sequence 13 AA;

Query Match 30.6%; Score 30; DB 5; Length 13;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy          7 EKPDLQP 13
              :|||::|
Db          1 QKPDMKP 7
```

RESULT 44
AAG88540
ID AAG88540 standard; peptide; 15 AA.
XX
AC AAG88540;
XX
DT 11-SEP-2001 (first entry)
XX
DE HER2/NEU DR supermotif binding peptide exemplary sequence #126.
XX
KW Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200141787-A1.
XX
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000WO-US033591.
XX
PR 10-DEC-1999; 99US-00458299.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
PI Keogh E;
XX
DR WPI; 2001-374995/39.
XX
PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing
PT cellular immune responses for the prevention and treatment of cancer.
XX
PS Disclosure; Page 170; 199pp; English.
XX
CC The present invention describes isolated prepared HER2/neu epitopes (I).
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is
CC culture in vitro and binds to a complex of an epitope (I), bound to a
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)
CC and a second epitope and the peptide is less than 50 contiguous amino
CC acids that have 100% identity with a native peptide sequence of HER2/neu;
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)
CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and
CC immunostimulant activities, and can be used in vaccines. (I), (II) and
CC (III) are useful for inducing cellular immune responses for the
CC prevention and treatment of cancer. (I) and (II) are useful for
CC monitoring or evaluating an immune response to a tumour-associated
CC antigen when incubated with a T lymphocyte sample form a patient and

CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope
CC based vaccines mean that immunosuppressive epitopes that may be present
CC in whole antigens may be avoided. Selected epitopes may be combined to
CC enhance immunogenicity. The possible pathological side effects caused by
CC infectious agents or whole protein antigen is eliminated. The vaccine
CC provides the ability to direct and focus an immune response to multiple
CC selected antigens from the same pathogen. Epitope-based anti-tumour
CC vaccines provides the opportunity to combine epitopes derived from
CC multiple tumour-associated molecules addressing the problem of tumour-
CC tumour variability and reducing the likelihood of tumour escape due to
CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 15 AA;

Query Match 30.6%; Score 30; DB 4; Length 15;
Best Local Similarity 45.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```
Qy          3 PPDVEKPDLQP 13
              |  | :||::|
Db          1 PEYVNQPDVRP 11
```

RESULT 45
ABR30154
ID ABR30154 standard; peptide; 15 AA.
XX
AC ABR30154;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 74P3B3 HLA peptide #2998.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
PT New composition comprising a substance that modulates the structure of

PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 469; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 15 AA;

Query Match 30.6%; Score 30; DB 6; Length 15;
Best Local Similarity 30.8%; Pred. No. 1.3e+03;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

```
Qy          3 PPDVEKPDLQPFQ 15
              || :::  |:|::
Db          2 PPPIKQCSLEPWR 14
```

RESULT 46
ADE70385
ID ADE70385 standard; peptide; 15 AA.
XX
AC ADE70385;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 4390.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;

XX
DR WPI; 2003-441560/41.
XX
PT A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
XX
PS Claim 13; Page 178; 135pp; English.
XX
CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 15 AA;

Query Match 30.6%; Score 30; DB 7; Length 15;
Best Local Similarity 38.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

```
Qy          3 PPDVEKPDLQPFQ 15
              |   || :::||:
Db          2 PSFKEKTEVEPFE 14
```

RESULT 47
ADE70790
ID ADE70790 standard; peptide; 15 AA.
XX
AC ADE70790;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 4795.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.

XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;
XX
DR WPI; 2003-441560/41.
XX
PT A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
XX
PS Claim 13; Page 182; 135pp; English.
XX
CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 15 AA;

Query Match 30.6%; Score 30; DB 7; Length 15;
Best Local Similarity 38.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

```
Qy          3 PPDVEKPDLQPFQ 15
              |   || :::||:
Db          2 PSFKEKTEVEPFE 14
```

RESULT 48
ADE70192
ID ADE70192 standard; peptide; 15 AA.
XX
AC ADE70192;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 4197.
XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.

PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;
XX
DR WPI; 2003-441560/41.
XX
PT A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
XX
PS Claim 13; Page 177; 135pp; English.
XX
CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 15 AA;

  Query Match   30.6%; Score 30; DB 7; Length 15;
  Best Local Similarity   38.5%; Pred. No. 1.3e+03;
  Matches   5; Conservative   4; Mismatches   4; Indels   0; Gaps   0;

```
Qy          3 PPDVEKPDLQPFQ 15
              |   || :::||:
Db          2 PSFKEKTEVEPFE 14
```

RESULT 49
AAU01833
ID AAU01833 standard; peptide; 17 AA.
XX
AC AAU01833;
XX
DT 07-SEP-2001 (first entry)
XX
DE Wheat Gliadin peptide J.
XX
KW Wheat; A-gliadin; peptide J; coeliac disease; gluten intolerance;
KW T-cell binding; antagonist; transglutaminase; transgenic plant.
XX
OS Triticum aestivum.
XX
PN WO200125793-A2.
XX
PD 12-APR-2001.

XX
PF 02-OCT-2000; 2000WO-GB003760.
XX
PR 01-OCT-1999; 99GB-00023306.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Anderson RP, Hill AVS, Jewell DP;
XX
DR WPI; 2001-300179/31.
XX
PT Diagnosing coeliac disease or susceptibility to the disease in an
PT individual, by detecting in vitro or in vivo T cells which bind
PT immunodominant T cell epitope obtained from naturally occurring homolog
PT of gliadin.
XX
PS Example 8; Fig 14; 107pp; English.
XX
CC The sequence represents wheat Gliadin peptide J, corresponding to A-
CC gliadin 57-73 and containing a natural polymorphism. The peptides of the
CC invention are used to test mammalian (preferably human) susceptibility to
CC coeliac disease (gluten intolerance). The peptides are contacted with a
CC blood sample and T cell recognition measured, a positive T-cell
CC recognition indicating a susceptibility to coeliac disease. The peptides
CC are useful for inducing tolerance in an individual and antagonists to the
CC peptides are useful for treating or preventing coeliac disease in an
CC individual and for producing an antibody specific to them or a wild-type
CC sequence. A mutant gliadin protein (or its fragment of 15 amino acids in
CC length) whose wild-type sequence can be modified by transglutaminase to a
CC sequence that comprises the epitope, but which has been modified in such
CC a way that it does not contain sequence which can be modified by
CC transglutaminase to a sequence that comprise the epitope is useful for
CC decreasing the ability of gliadin protein to cause Coeliac disease.
CC Nucleic acids encoding proteins antagonistic to the T-cell binding of the
CC epitopes are useful for obtaining a transgenic plant cell or seed and for
CC the production of a protein. The resultant crop plant is useful for
CC obtaining a product of a wheat plant, especially grain, which is
CC optionally processed into flour or another grain product. Food comprising
CC the antagonistic protein is useful instead of a wild-type gliadin
XX
SQ Sequence 17 AA;

Query Match 30.6%; Score 30; DB 4; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```
Qy          3 PPDVEKPDLQP 13
              || :  |  ||
Db          7 PPQLPYPQTQP 17
```

RESULT 50
AAU01822
ID AAU01822 standard; peptide; 17 AA.
XX
AC AAU01822;
XX

DT 07-SEP-2001 (first entry)
XX
DE Wheat Gliadin peptide O.
XX
KW Wheat; A-gliadin; peptide O; coeliac disease; gluten intolerance;
KW T-cell binding; antagonist; transglutaminase; transgenic plant.
XX
OS Triticum aestivum.
XX
PN WO200125793-A2.
XX
PD 12-APR-2001.
XX
PF 02-OCT-2000; 2000WO-GB003760.
XX
PR 01-OCT-1999; 99GB-00023306.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Anderson RP, Hill AVS, Jewell DP;
XX
DR WPI; 2001-300179/31.
XX
PT Diagnosing coeliac disease or susceptibility to the disease in an
PT individual, by detecting in vitro or in vivo T cells which bind
PT immunodominant T cell epitope obtained from naturally occurring homolog
PT of gliadin.
XX
PS Example 8; Fig 14; 107pp; English.
XX
CC The sequence represents wheat Gliadin peptide O, corresponding to A-
CC gliadin 57-73 and containing a natural polymorphism. The peptides of the
CC invention are used to test mammalian (preferably human) susceptibility to
CC coeliac disease (gluten intolerance). The peptides are contacted with a
CC blood sample and T cell recognition measured, a positive T-cell
CC recognition indicating a susceptibility to coeliac disease. The peptides
CC are useful for inducing tolerance in an individual and antagonists to the
CC peptides are useful for treating or preventing coeliac disease in an
CC individual and for producing an antibody specific to them or a wild-type
CC sequence. A mutant gliadin protein (or its fragment of 15 amino acids in
CC length) whose wild-type sequence can be modified by transglutaminase to a
CC sequence that comprises the epitope, but which has been modified in such
CC a way that it does not contain sequence which can be modified by
CC transglutaminase to a sequence that comprise the epitope is useful for
CC decreasing the ability of gliadin protein to cause Coeliac disease.
CC Nucleic acids encoding proteins antagonistic to the T-cell binding of the
CC epitopes are useful for obtaining a transgenic plant cell or seed and for
CC the production of a protein. The resultant crop plant is useful for
CC obtaining a product of a wheat plant, especially grain, which is
CC optionally processed into flour or another grain product. Food comprising
CC the antagonistic protein is useful instead of a wild-type gliadin
XX
SQ Sequence 17 AA;

Query Match 30.6%; Score 30; DB 4; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```
Qy          3 PPDVEKPDLQP 13
              || :  |  ||
Db          7 PPQLPYPQTQP 17
```

Search completed: July 4, 2004, 04:40:39
Job time : 46.1791 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:37:26 ; Search time 11.2836 Seconds
(without alignments)
82.356 Million cell updates/sec

Title: US-09-641-802-3
Perfect score: 98
Sequence: 1 DQPPDVEKPDLQPFQVQS 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 121837

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	98	100.0	18	4	US-09-641-803-3	Sequence 3, Appli
2	33	33.7	14	2	US-07-963-538B-10	Sequence 10, Appl
3	33	33.7	18	2	US-08-769-745-20	Sequence 20, Appl
4	32	32.7	18	3	US-08-602-999A-305	Sequence 305, App
5	32	32.7	18	4	US-09-500-124-305	Sequence 305, App
6	31	31.6	17	1	US-08-318-200-21	Sequence 21, Appl
7	31	31.6	18	1	US-08-336-618-11	Sequence 11, Appl
8	30.5	31.1	11	2	US-08-343-443B-74	Sequence 74, Appl
9	30.5	31.1	11	2	US-08-343-443B-94	Sequence 94, Appl
10	29	29.6	15	4	US-09-914-259-70	Sequence 70, Appl
11	29	29.6	17	1	US-08-144-121-12	Sequence 12, Appl

12	29	29.6	17	2	US-08-735-893-12	Sequence 12, Appl
13	29	29.6	18	3	US-09-461-697-200	Sequence 200, App
14	28	28.6	12	1	US-08-190-788A-43	Sequence 43, Appl
15	28	28.6	12	1	US-08-190-788A-52	Sequence 52, Appl
16	28	28.6	12	1	US-08-190-788A-284	Sequence 284, App
17	28	28.6	12	1	US-08-383-474B-48	Sequence 48, Appl
18	28	28.6	12	1	US-08-383-474B-57	Sequence 57, Appl
19	28	28.6	12	1	US-08-383-474B-285	Sequence 285, App
20	28	28.6	12	1	US-08-465-391A-43	Sequence 43, Appl
21	28	28.6	12	1	US-08-465-391A-52	Sequence 52, Appl
22	28	28.6	12	1	US-08-465-391A-284	Sequence 284, App
23	28	28.6	12	2	US-08-464-538B-43	Sequence 43, Appl
24	28	28.6	12	2	US-08-464-538B-52	Sequence 52, Appl
25	28	28.6	12	2	US-08-464-538B-283	Sequence 283, App
26	28	28.6	12	2	US-08-463-076E-87	Sequence 87, Appl
27	28	28.6	12	2	US-08-463-076E-96	Sequence 96, Appl
28	28	28.6	12	2	US-08-463-076E-357	Sequence 357, App
29	28	28.6	12	4	US-09-428-082B-673	Sequence 673, App
30	28	28.6	12	4	US-09-428-082B-683	Sequence 683, App
31	28	28.6	12	4	US-09-428-082B-958	Sequence 958, App
32	28	28.6	13	2	US-08-347-335A-13	Sequence 13, Appl
33	28	28.6	15	1	US-08-467-083-53	Sequence 53, Appl
34	28	28.6	15	1	US-08-414-417B-53	Sequence 53, Appl
35	28	28.6	15	2	US-08-486-348A-53	Sequence 53, Appl
36	28	28.6	15	2	US-08-468-545B-53	Sequence 53, Appl
37	28	28.6	15	3	US-08-466-680B-53	Sequence 53, Appl
38	28	28.6	15	4	US-09-354-533-53	Sequence 53, Appl
39	28	28.6	16	1	US-08-190-788A-170	Sequence 170, App
40	28	28.6	16	1	US-08-383-474B-173	Sequence 173, App
41	28	28.6	16	1	US-08-465-391A-170	Sequence 170, App
42	28	28.6	16	2	US-08-464-538B-170	Sequence 170, App
43	28	28.6	16	2	US-08-463-076E-223	Sequence 223, App
44	28	28.6	16	4	US-09-428-082B-786	Sequence 786, App
45	28	28.6	17	1	US-08-190-788A-169	Sequence 169, App
46	28	28.6	17	1	US-08-190-788A-230	Sequence 230, App
47	28	28.6	17	1	US-08-190-788A-233	Sequence 233, App
48	28	28.6	17	1	US-08-190-788A-234	Sequence 234, App
49	28	28.6	17	1	US-08-383-474B-172	Sequence 172, App
50	28	28.6	17	1	US-08-383-474B-233	Sequence 233, App
51	28	28.6	17	1	US-08-383-474B-236	Sequence 236, App
52	28	28.6	17	1	US-08-383-474B-237	Sequence 237, App
53	28	28.6	17	1	US-08-465-391A-169	Sequence 169, App
54	28	28.6	17	1	US-08-465-391A-230	Sequence 230, App
55	28	28.6	17	1	US-08-465-391A-233	Sequence 233, App
56	28	28.6	17	1	US-08-465-391A-234	Sequence 234, App
57	28	28.6	17	2	US-08-464-538B-169	Sequence 169, App
58	28	28.6	17	2	US-08-464-538B-230	Sequence 230, App
59	28	28.6	17	2	US-08-464-538B-233	Sequence 233, App
60	28	28.6	17	2	US-08-464-538B-234	Sequence 234, App
61	28	28.6	17	2	US-08-463-076E-222	Sequence 222, App
62	28	28.6	17	2	US-08-463-076E-284	Sequence 284, App
63	28	28.6	17	2	US-08-463-076E-287	Sequence 287, App
64	28	28.6	17	2	US-08-463-076E-288	Sequence 288, App
65	28	28.6	17	3	US-08-602-999A-338	Sequence 338, App
66	28	28.6	17	4	US-09-500-124-338	Sequence 338, App
67	28	28.6	17	4	US-09-428-082B-785	Sequence 785, App
68	28	28.6	17	4	US-09-428-082B-844	Sequence 844, App

69	28	28.6	17	4	US-09-428-082B-847	Sequence 847, App
70	28	28.6	17	4	US-09-428-082B-848	Sequence 848, App
71	27	27.6	8	1	US-07-923-724-48	Sequence 48, Appl
72	27	27.6	8	2	US-08-609-426A-48	Sequence 48, Appl
73	27	27.6	8	2	US-08-374-652C-38	Sequence 38, Appl
74	27	27.6	9	2	US-08-146-028-431	Sequence 431, App
75	27	27.6	9	2	US-08-146-028-432	Sequence 432, App
76	27	27.6	9	2	US-08-146-028-433	Sequence 433, App
77	27	27.6	9	3	US-08-723-425A-431	Sequence 431, App
78	27	27.6	9	3	US-08-723-425A-432	Sequence 432, App
79	27	27.6	9	3	US-08-723-425A-433	Sequence 433, App
80	27	27.6	9	3	US-09-112-206-431	Sequence 431, App
81	27	27.6	9	3	US-09-112-206-432	Sequence 432, App
82	27	27.6	9	3	US-09-112-206-433	Sequence 433, App
83	27	27.6	9	3	US-09-518-046-148	Sequence 148, App
84	27	27.6	9	4	US-09-790-497A-379	Sequence 379, App
85	27	27.6	9	4	US-09-790-497A-380	Sequence 380, App
86	27	27.6	9	4	US-09-790-497A-381	Sequence 381, App
87	27	27.6	9	4	US-09-790-497A-564	Sequence 564, App
88	27	27.6	9	4	US-09-790-497A-565	Sequence 565, App
89	27	27.6	9	4	US-09-790-497A-566	Sequence 566, App
90	27	27.6	9	4	US-09-576-824A-379	Sequence 379, App
91	27	27.6	9	4	US-09-576-824A-380	Sequence 380, App
92	27	27.6	9	4	US-09-576-824A-381	Sequence 381, App
93	27	27.6	10	3	US-08-762-428A-1	Sequence 1, Appli
94	27	27.6	11	4	US-09-576-824A-564	Sequence 564, App
95	27	27.6	11	4	US-09-576-824A-565	Sequence 565, App
96	27	27.6	11	4	US-09-576-824A-566	Sequence 566, App
97	27	27.6	11	4	US-09-576-824A-567	Sequence 567, App
98	27	27.6	12	1	US-08-190-788A-162	Sequence 162, App
99	27	27.6	12	1	US-08-383-474B-165	Sequence 165, App
100	27	27.6	12	1	US-08-465-391A-162	Sequence 162, App

ALIGNMENTS

```
RESULT 1
US-09-641-803-3
; Sequence 3, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
;  APPLICANT:  STANTON, G. John
;  APPLICANT:  HUGHES, Thomas K.
;  APPLICANT:  BOLDOGH, Istvan
;  TITLE OF INVENTION:  USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
;  TITLE OF INVENTION:  ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
;  FILE REFERENCE:  265.00220101
;  CURRENT APPLICATION NUMBER: US/09/641,803
;  CURRENT FILING DATE:  2000-08-17
;  PRIOR APPLICATION NUMBER:  60/149,310
;  PRIOR FILING DATE:  1999-08-17
;  NUMBER OF SEQ ID NOS:  34
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 18
;   TYPE: PRT
```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-3

  Query Match   100.0%; Score 98; DB 4; Length 18;
  Best Local Similarity   100.0%; Pred. No. 9.8e-09;
  Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 DQPPDVEKPDLQPFQVQS 18
              ||||||||||||||||||
Db   1 DQPPDVEKPDLQPFQVQS 18

RESULT 2
US-07-963-538B-10
; Sequence 10, Application US/07963538B
; Patent No. 5851983
; GENERAL INFORMATION:
;   APPLICANT: SUGIYAMA, TAKASHI
;   APPLICANT: KAMIMURA, TAKASHI
;   APPLICANT: MASUDA, KENICHI
;   APPLICANT: OKADA, MASAHIRO
;   APPLICANT: OHTSUKA, EIKO
;   APPLICANT: IMAIZUMI, ATSUSHI
;   APPLICANT: WATANABE, KUNIHITO
;   APPLICANT: SUGA, TETSUYA
;   APPLICANT: MATSUMOTO, YOHICHI
;   APPLICANT: TAKEUCHI, AKIKO
;   TITLE OF INVENTION: ELASTASE INHIBITORY POLYPEPTIDE AND
;   TITLE OF INVENTION: PROCESS FOR PRODUCTION THEREOF BY RECOMBINANT GENE
;   TITLE OF INVENTION: TECHNOLOGY
;   NUMBER OF SEQUENCES: 36
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: COOLEY GODWARD LLP
;   STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
;   CITY: PALO ALTO
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94306-2155
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/963,538B
;   FILING DATE: 20-OCT-1992
;   CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/843,359
;   FILING DATE: 25-FEB-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/408,483
;   FILING DATE: 22-AUG-1989
;   PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 4-212399
; FILING DATE: 17-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-212398
; FILING DATE: 17-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-355553
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 62-330219
; FILING DATE: 28-DEC-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: NEELEY PH.D., RICHARD L.
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: TEJN-005/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5070
; TELEFAX: 415-857-0663
; TELEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-963-538B-10

Query Match 33.7%; Score 33; DB 2; Length 14;
Best Local Similarity 53.8%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 DQPPDVEKPDLQP 13
              | || ||   | |
Db          1 DDPPTVELQGLVP 13
```

RESULT 3
US-08-769-745-20
; Sequence 20, Application US/08769745
; Patent No. 5955259
; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd C.
; APPLICANT: Levitan, Irwin B.
; APPLICANT: Brandeis University
; TITLE OF INVENTION: Mechanism for the Regulation of Ion
; TITLE OF INVENTION: Channel Activity
; FILE REFERENCE: BRU96-02
; CURRENT APPLICATION NUMBER: US/08/769,745
; CURRENT FILING DATE: 1996-12-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Rat
US-08-769-745-20

Query Match 33.7%; Score 33; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```
Qy          2 QPPDVEKPDLQP 13
              |||:   | | |
Db          6 QPPESSPPPLLP 17
```

RESULT 4
US-08-602-999A-305
; Sequence 305, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 305:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-305

Query Match 32.7%; Score 32; DB 3; Length 18;

```
  Best Local Similarity   43.8%;  Pred. No. 1e+02;
  Matches    7;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          2 QPPDVEKPDLQPFQVQ 17
              |||    |  ||   |
Db          3 QPPYFPPPPYQPIYPQ 18


RESULT 5
US-09-500-124-305
; Sequence 305, Application US/09500124
; Patent No. 6432920
;  GENERAL INFORMATION:
;    APPLICANT:  SPARKS, Andrew B.
;    APPLICANT:  KAY, Brian K.
;    APPLICANT:  THORN, Judith M.
;    APPLICANT:  QUILLIAM, Lawrence A.
;    APPLICANT:  DER, Channing J.
;    APPLICANT:  FOWLKES, Dana M.
;    APPLICANT:  RIDER, James E.
;    TITLE OF INVENTION:  SH3 BINDING PEPTIDES AND METHODS OF
;    TITLE OF INVENTION:  ISOLATING AND USING SAME
;    NUMBER OF SEQUENCES:  467
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/500,124
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/602,999
;      FILING DATE:  16-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  1101-202
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  305:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-09-500-124-305
```

```
  Query Match             32.7%;  Score 32;  DB 4;  Length 18;
  Best Local Similarity   43.8%;  Pred. No. 1e+02;
  Matches    7;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          2 QPPDVEKPDLQPFQVQ 17
              |||    |  ||   |
Db          3 QPPYFPPPPYQPIYPQ 18


RESULT 6
US-08-318-200-21
; Sequence 21, Application US/08318200
; Patent No. 5578496
;  GENERAL INFORMATION:
;    APPLICANT:  Atassi, M. Z.
;    APPLICANT:  Ashizawa, T.
;    TITLE OF INVENTION:  N-TERMINAL PVA- OR PEG-CONJUGATED
;    TITLE OF INVENTION:  PEPTIDES FOR EPITOPE-SPECIFIC IMMUNOSUPPRESSION
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  PO Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,200
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/965,670
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDaniel, C. Steven
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713-787-1400
;      TELEFAX:  713-789-2679
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-318-200-21

  Query Match             31.6%;  Score 31;  DB 1;  Length 17;
  Best Local Similarity   45.5%;  Pred. No. 1.3e+02;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 PDVEKPDLQPF 14
```

```
              |: ::|||  |
Db          3 PESDQPDLSNF 13


RESULT 7
US-08-336-618-11
; Sequence 11, Application US/08336618
; Patent No. 5763590
;  GENERAL INFORMATION:
;    APPLICANT:  Peattie, Debra A.
;    APPLICANT:  Harding, Matthew W.
;    APPLICANT:  Livingston, David J.
;    TITLE OF INVENTION:  ISOLATION OF AN Mr 52,000 FK506 BINDING
;    TITLE OF INVENTION:  PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
;    TITLE OF INVENTION:  cDNA
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith and Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/336,618
;      FILING DATE:  09-NOV-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/963,325
;      FILING DATE:  16-OCT-1992
;      APPLICATION NUMBER:  US 07/777,752
;      FILING DATE:  11-OCT-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/
;      FILING DATE:  09-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  VPI91-06A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-336-618-11

  Query Match             31.6%;  Score 31;  DB 1;  Length 18;
  Best Local Similarity   60.0%;  Pred. No. 1.4e+02;
```

Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 DQPPDVEKPD 10
              ||| | |  |
Db          7 DQPADAEMRD 16
```

RESULT 8
US-08-343-443B-74
; Sequence 74, Application US/08343443B
; Patent No. 5968734
; GENERAL INFORMATION:
; APPLICANT: Aurias, Alain
; APPLICANT: Delattre, Olivier
; APPLICANT: Desmaze, Chantal
; APPLICANT: Melot, Thomas
; APPLICANT: Peter, Martine
; APPLICANT: Ploougastel, Beatrice
; APPLICANT: Thomas, Gilles
; APPLICANT: Zucman, Jessica
; TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
; TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
; TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF
CANCEROUS
; TITLE OF INVENTION: TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM
SAID
; TITLE OF INVENTION: TRANSLOCATIONS
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weiser & Associates
; STREET: 230 South Fifteenth Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: AEDIT 1.0 DOS text editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,443B
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR93/00494
; FILING DATE: 19-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/06123
; FILING DATE: 20-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 989.6121P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394

```
;  INFORMATION FOR SEQ ID NO:  74:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  11 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-343-443B-74

  Query Match             31.1%;  Score 30.5;  DB 2;  Length 11;
  Best Local Similarity   46.2%;  Pred. No. 98;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    3;  Gaps    1;

Qy          4 PDVEKPDLQPFQV 16
              ||:   || |:|:
Db          1 PDL---DLDPYQI 10


RESULT 9
US-08-343-443B-94
; Sequence 94, Application US/08343443B
; Patent No. 5968734
;  GENERAL INFORMATION:
;     APPLICANT:  Aurias, Alain
;     APPLICANT:  Delattre, Olivier
;     APPLICANT:  Desmaze, Chantal
;     APPLICANT:  Melot, Thomas
;     APPLICANT:  Peter, Martine
;     APPLICANT:  Plougastel, Beatrice
;     APPLICANT:  Thomas, Gilles
;     APPLICANT:  Zucman, Jessica
;     TITLE OF INVENTION:  NUCLEIC ACID CORRESPONDING TO A GENE OF
;     TITLE OF INVENTION:  CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
;     TITLE OF INVENTION:  TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF
CANCEROUS
;     TITLE OF INVENTION:  TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM
SAID
;     TITLE OF INVENTION:  TRANSLOCATIONS
;     NUMBER OF SEQUENCES:  129
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Weiser & Associates
;       STREET:  230 South Fifteenth Street
;       CITY:  Philadelphia
;       STATE:  PA
;       COUNTRY:  USA
;       ZIP:  19102
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  AEDIT 1.0 DOS text editor
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/343,443B
;       FILING DATE:  18-NOV-1994
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/FR93/00494
;       FILING DATE:  19-MAY-1993
```

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 92/06123
;      FILING DATE:  20-MAY-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weiser, Gerard J.
;      REGISTRATION NUMBER:  19,763
;      REFERENCE/DOCKET NUMBER:  989.6121P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-875-8383
;      TELEFAX:  215-875-8394
;  INFORMATION FOR SEQ ID NO:  94:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-343-443B-94

  Query Match             31.1%;  Score 30.5;  DB 2;  Length 11;
  Best Local Similarity   46.2%;  Pred. No. 98;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    3;  Gaps    1;

Qy          4 PDVEKPDLQPFQV 16
              ||:   || |:|:
Db          1 PDL---DLDPYQI 10


RESULT 10
US-09-914-259-70
; Sequence 70, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
;  APPLICANT: Makowski, Lee
;  APPLICANT:  Hyman, Paul
;  APPLICANT:  Williams, Mark
;  TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
;  FILE REFERENCE: 8471-010-999
;  CURRENT APPLICATION NUMBER: US/09/914,259
;  CURRENT FILING DATE:  2000-11-21
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 70
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: human rhinovirus 2
US-09-914-259-70

  Query Match             29.6%;  Score 29;  DB 4;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 PDLQP 13
              |||||
Db          9 PDLQP 13


RESULT 11
```

US-08-144-121-12
; Sequence 12, Application US/08144121
; Patent No. 5610031
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert E.
; APPLICANT: Wagman, David W.
; TITLE OF INVENTION: B1k CHAIN OF LAMININ AND METHODS OF USE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: United States
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/144,121
; FILING DATE: 27-OCT-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: (MGH-0780.0) MGP-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-144-121-12

Query Match 29.6%; Score 29; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 DQPPDVEKPD 10
              |: ||:|  |
Db          1 DENPDIECAD 10
```

RESULT 12
US-08-735-893-12
; Sequence 12, Application US/08735893
; Patent No. 5914317
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert E.
; APPLICANT: Wagman, David W.
; TITLE OF INVENTION: B1k CHAIN OF LAMININ AND METHODS OF USE

```
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street, suite 510
;      CITY:  BOSTON
;      STATE:  Massachusetts
;      COUNTRY:  United States
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/735,893
;      FILING DATE:  18-OCT-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/144,121
;      FILING DATE:  27-OCT-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Myers, Paul L.
;      REGISTRATION NUMBER:  35,965
;      REFERENCE/DOCKET NUMBER:  (MGH-0780.1) MGP-021DV
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
US-08-735-893-12

  Query Match             29.6%;  Score 29;  DB 2;  Length 17;
  Best Local Similarity   50.0%;  Pred. No. 2.7e+02;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DQPPDVEKPD 10
              |: ||:|  |
Db          1 DENPDIECAD 10


RESULT 13
US-09-461-697-200
; Sequence 200, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
;  APPLICANT: COGENT NEUROSCIENCE, Inc.
;  APPLICANT: Lo, Donald C.
;  APPLICANT: Barney, Shawn
;  APPLICANT: Thomas, Mary Beth
;  APPLICANT: Portbury, Stuart D.
;  APPLICANT: Puranam, Kasturi
```

```
;  APPLICANT: Katz, Lawrence C.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
;  TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
;  TITLE OF INVENTION: CELL DEATH
;  FILE REFERENCE: 10001-005-999
;  CURRENT APPLICATION NUMBER: US/09/461,697
;  CURRENT FILING DATE: 1999-12-14
;  NUMBER OF SEQ ID NOS: 466
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 200
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-461-697-200

  Query Match             29.6%;  Score 29;  DB 3;  Length 18;
  Best Local Similarity   54.5%;  Pred. No. 2.8e+02;
  Matches    6;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 VEKPDLQPFQV 16
              :||| ||  |:
Db          1 MEKPKLQRHQL 11


RESULT 14
US-08-190-788A-43
; Sequence 43, Application US/08190788A
; Patent No. 5608035
;  GENERAL INFORMATION:
;    APPLICANT:  Yanofsky, Stephen D.
;    APPLICANT:  Barrett, Ronald W.
;    APPLICANT:  Baldwin, David N.
;    APPLICANT:  Jacobs, Jeff W.
;    TITLE OF INVENTION:  Peptides and Compounds That Bind to the
;    TITLE OF INVENTION:  IL-1 Receptor
;    NUMBER OF SEQUENCES:  312
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Affymax Technologies N.V.
;      STREET:  4001 Miranda Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/190,788A
;      FILING DATE:  02-FEB-1994
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/847,567
;      FILING DATE:  05-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stevens, Lauren L.
```

```
;       REGISTRATION NUMBER:  36,691
;       REFERENCE/DOCKET NUMBER:  1019.1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-496-2300
;       TELEFAX:  415-424-0832
;   INFORMATION FOR SEQ ID NO:  43:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  12 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-190-788A-43

  Query Match           28.6%;  Score 28;  DB 1;  Length 12;
  Best Local Similarity  71.4%;  Pred. No. 2.6e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 QPFQVQS 18
                ||: |||
Db          6 QPYSVQS 12


RESULT 15
US-08-190-788A-52
; Sequence 52, Application US/08190788A
; Patent No. 5608035
;  GENERAL INFORMATION:
;    APPLICANT:  Yanofsky, Stephen D.
;    APPLICANT:  Barrett, Ronald W.
;    APPLICANT:  Baldwin, David N.
;    APPLICANT:  Jacobs, Jeff W.
;    TITLE OF INVENTION:  Peptides and Compounds That Bind to the
;    TITLE OF INVENTION:  IL-1 Receptor
;    NUMBER OF SEQUENCES:  312
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Affymax Technologies N.V.
;      STREET:  4001 Miranda Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/190,788A
;      FILING DATE:  02-FEB-1994
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/847,567
;      FILING DATE:  05-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stevens, Lauren L.
;      REGISTRATION NUMBER:  36,691
```

```
;       REFERENCE/DOCKET NUMBER:  1019.1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-496-2300
;       TELEFAX:  415-424-0832
;   INFORMATION FOR SEQ ID NO:  52:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  12 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-190-788A-52

  Query Match             28.6%;  Score 28;  DB 1;  Length 12;
  Best Local Similarity   71.4%;  Pred. No. 2.6e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 QPFQVQS 18
               ||: |||
Db           6 QPYSVQS 12


RESULT 16
US-08-190-788A-284
; Sequence 284, Application US/08190788A
; Patent No. 5608035
;  GENERAL INFORMATION:
;     APPLICANT:  Yanofsky, Stephen D.
;     APPLICANT:  Barrett, Ronald W.
;     APPLICANT:  Baldwin, David N.
;     APPLICANT:  Jacobs, Jeff W.
;     TITLE OF INVENTION:  Peptides and Compounds That Bind to the
;     TITLE OF INVENTION:  IL-1 Receptor
;     NUMBER OF SEQUENCES:  312
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Affymax Technologies N.V.
;       STREET:  4001 Miranda Avenue
;       CITY:  Palo Alto
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94304
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/190,788A
;       FILING DATE:  02-FEB-1994
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/847,567
;       FILING DATE:  05-MAR-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Stevens, Lauren L.
;       REGISTRATION NUMBER:  36,691
;       REFERENCE/DOCKET NUMBER:  1019.1
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-496-2300
;      TELEFAX:  415-424-0832
;  INFORMATION FOR SEQ ID NO:  284:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Region
;      LOCATION:  5
;      OTHER INFORMATION:  /note= "naphthylalanine."
US-08-190-788A-284

  Query Match             28.6%;  Score 28;  DB 1;  Length 12;
  Best Local Similarity   71.4%;  Pred. No. 2.6e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 QPFQVQS 18
              ||: |||
Db          6 QPYSVQS 12


RESULT 17
US-08-383-474B-48
; Sequence 48, Application US/08383474B
; Patent No. 5767234
;  GENERAL INFORMATION:
;    APPLICANT:  Yanofsky, Stephen D.
;    APPLICANT:  Barrett, Ronald W.
;    APPLICANT:  Baldwin, David N.
;    APPLICANT:  Jacobs, Jeff W.
;    TITLE OF INVENTION:  Peptides and Compounds That Bind to
;    TITLE OF INVENTION:  the IL-1 Receptor
;    NUMBER OF SEQUENCES:  314
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend & Townsend & Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/383,474B
;      FILING DATE:  01-FEB-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/190,788
;      FILING DATE:  02-FEB-1994
;      CLASSIFICATION:  530
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stevens, Lauren L.
;      REGISTRATION NUMBER:  36,691
;      REFERENCE/DOCKET NUMBER:  1019.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-496-2300
;      TELEFAX:  415-424-0832
;  INFORMATION FOR SEQ ID NO:  48:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-383-474B-48

  Query Match             28.6%;  Score 28;  DB 1;  Length 12;
  Best Local Similarity   71.4%;  Pred. No. 2.6e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 QPFQVQS 18
                ||: |||
Db          6 QPYSVQS 12


RESULT 18
US-08-383-474B-57
; Sequence 57, Application US/08383474B
; Patent No. 5767234
;  GENERAL INFORMATION:
;    APPLICANT:  Yanofsky, Stephen D.
;    APPLICANT:  Barrett, Ronald W.
;    APPLICANT:  Baldwin, David N.
;    APPLICANT:  Jacobs, Jeff W.
;    TITLE OF INVENTION:  Peptides and Compounds That Bind to
;    TITLE OF INVENTION:  the IL-1 Receptor
;    NUMBER OF SEQUENCES:  314
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend & Townsend & Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/383,474B
;      FILING DATE:  01-FEB-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/190,788
;      FILING DATE:  02-FEB-1994
;      CLASSIFICATION:  530
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stevens, Lauren L.
;      REGISTRATION NUMBER:  36,691
;      REFERENCE/DOCKET NUMBER:  1019.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-496-2300
;      TELEFAX:  415-424-0832
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-383-474B-57

  Query Match             28.6%;  Score 28;  DB 1;  Length 12;
  Best Local Similarity   71.4%;  Pred. No. 2.6e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 QPFQVQS 18
                ||: |||
Db          6 QPYSVQS 12


RESULT 19
US-08-383-474B-285
; Sequence 285, Application US/08383474B
; Patent No. 5767234
;  GENERAL INFORMATION:
;    APPLICANT:  Yanofsky, Stephen D.
;    APPLICANT:  Barrett, Ronald W.
;    APPLICANT:  Baldwin, David N.
;    APPLICANT:  Jacobs, Jeff W.
;    TITLE OF INVENTION:  Peptides and Compounds That Bind to
;    TITLE OF INVENTION:  the IL-1 Receptor
;    NUMBER OF SEQUENCES:  314
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend & Townsend & Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/383,474B
;      FILING DATE:  01-FEB-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/190,788
;      FILING DATE:  02-FEB-1994
;      CLASSIFICATION:  530
```

```
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Stevens, Lauren L.
;       REGISTRATION NUMBER:  36,691
;       REFERENCE/DOCKET NUMBER:  1019.3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-496-2300
;       TELEFAX:  415-424-0832
;   INFORMATION FOR SEQ ID NO:  285:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  12 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FEATURE:
;       NAME/KEY:  Region
;       LOCATION:  5
;       OTHER INFORMATION:  /note= "naphthylalanine."
US-08-383-474B-285

  Query Match             28.6%;  Score 28;  DB 1;  Length 12;
  Best Local Similarity   71.4%;  Pred. No. 2.6e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 QPFQVQS 18
                ||: |||
Db          6 QPYSVQS 12


RESULT 20
US-08-465-391A-43
; Sequence 43, Application US/08465391A
; Patent No. 5786331
;  GENERAL INFORMATION:
;     APPLICANT:  Barrett, Ronald W.
;     APPLICANT:  Yanofsky, Stephen D.
;     APPLICANT:  Baldwin, David
;     APPLICANT:  Jacobs, Jeff W.
;     APPLICANT:  Bovy, Phillipe R.
;     APPLICANT:  Leahy, Ellen M.
;     APPLICANT:  Pottorf, Richard S.
;     TITLE OF INVENTION:  Peptides and Compounds That Bind to the
;     TITLE OF INVENTION:  IL-1 Receptor
;     NUMBER OF SEQUENCES:  405
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend and Crew
;       STREET:  One Market Plaza, Steuart Tower, Suite 2000
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94105
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
```

; APPLICATION NUMBER: US/08/465,391A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5786331viel, Vern
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-391A-43

Query Match 28.6%; Score 28; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          12 QPFQVQS 18
               ||: |||
Db           6 QPYSVQS 12
```

RESULT 21
US-08-465-391A-52
; Sequence 52, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Phillipe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 405
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA

```
;       ZIP:  94105
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/465,391A
;       FILING DATE:  05-JUN-1995
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/373,474
;       FILING DATE:  01-FEB-1995
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/190,788
;       FILING DATE:  02-FEB-1994
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  No. 5786331viel, Vern
;       REGISTRATION NUMBER:  32,483
;       REFERENCE/DOCKET NUMBER:  16528A-001840/1019.2A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-326-2400
;       TELEFAX:  415-326-2422
;   INFORMATION FOR SEQ ID NO:  52:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  12 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-465-391A-52

  Query Match             28.6%;  Score 28;  DB 1;  Length 12;
  Best Local Similarity   71.4%;  Pred. No. 2.6e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 QPFQVQS 18
              ||: |||
Db          6 QPYSVQS 12


RESULT 22
US-08-465-391A-284
; Sequence 284, Application US/08465391A
; Patent No. 5786331
;  GENERAL INFORMATION:
;     APPLICANT:  Barrett, Ronald W.
;     APPLICANT:  Yanofsky, Stephen D.
;     APPLICANT:  Baldwin, David
;     APPLICANT:  Jacobs, Jeff W.
;     APPLICANT:  Bovy, Phillipe R.
;     APPLICANT:  Leahy, Ellen M.
;     APPLICANT:  Pottorf, Richard S.
;     TITLE OF INVENTION:  Peptides and Compounds That Bind to the
;     TITLE OF INVENTION:  IL-1 Receptor
```

```
;    NUMBER OF SEQUENCES:  405
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,391A
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/373,474
;      FILING DATE:  01-FEB-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/190,788
;      FILING DATE:  02-FEB-1994
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5786331viel, Vern
;      REGISTRATION NUMBER:  32,483
;      REFERENCE/DOCKET NUMBER:  16528A-001840/1019.2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  284:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Region
;      LOCATION:  5
;      OTHER INFORMATION:  /note= "naphthylalanine."
US-08-465-391A-284

  Query Match             28.6%;  Score 28;  DB 1;  Length 12;
  Best Local Similarity   71.4%;  Pred. No. 2.6e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 QPFQVQS 18
              ||: |||
Db          6 QPYSVQS 12


RESULT 23
US-08-464-538B-43
; Sequence 43, Application US/08464538B
```

; Patent No. 5861476
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Phillipe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,538B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 16528A-001810
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-464-538B-43

Query Match 28.6%; Score 28; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18

```
              ||: |||
Db          6 QPYSVQS 12


RESULT 24
US-08-464-538B-52
; Sequence 52, Application US/08464538B
; Patent No. 5861476
;  GENERAL INFORMATION:
;    APPLICANT:  Barrett, Ronald W.
;    APPLICANT:  Yanofsky, Stephen D.
;    APPLICANT:  Baldwin, David
;    APPLICANT:  Jacobs, Jeff W.
;    APPLICANT:  Bovy, Phillipe R.
;    APPLICANT:  Leahy, Ellen M.
;    APPLICANT:  Pottorf, Richard S.
;    TITLE OF INVENTION:  Peptides and Compounds That Bind to the
;    TITLE OF INVENTION:  IL-1 Receptor
;    NUMBER OF SEQUENCES:  402
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/464,538B
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/373,474
;      FILING DATE:  01-FEB-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/190,788
;      FILING DATE:  02-FEB-1994
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  16528A-001810
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  52:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
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US-08-464-538B-52

Query Match 28.6%; Score 28; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          12 QPFQVQS 18
               ||: |||
Db           6 QPYSVQS 12
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RESULT 25
US-08-464-538B-283
; Sequence 283, Application US/08464538B
; Patent No. 5861476
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Phillipe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,538B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 16528A-001810
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422

```
;  INFORMATION FOR SEQ ID NO:  283:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Region
;      LOCATION:  5
;      OTHER INFORMATION:  /note= "naphthylalanine."
US-08-464-538B-283

  Query Match             28.6%;  Score 28;  DB 2;  Length 12;
  Best Local Similarity   71.4%;  Pred. No. 2.6e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 QPFQVQS 18
              ||: |||
Db          6 QPYSVQS 12


RESULT 26
US-08-463-076E-87
; Sequence 87, Application US/08463076E
; Patent No. 5880096
;  GENERAL INFORMATION:
;    APPLICANT:  Barrett, Ronald W.
;    APPLICANT:  Yanofsky, Stephen D.
;    TITLE OF INVENTION:  Peptides and Compounds That Bind to the
;    TITLE OF INVENTION:  IL-1 Receptor
;    NUMBER OF SEQUENCES:  392
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,076E
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Snyder, Joseph R.
;      REGISTRATION NUMBER:  39,381
;      REFERENCE/DOCKET NUMBER:  16528A-001850US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  87:
;    SEQUENCE CHARACTERISTICS:
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; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-463-076E-87

Query Match 28.6%; Score 28; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy         12 QPFQVQS 18
              ||: |||
Db          6 QPYSVQS 12
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RESULT 27
US-08-463-076E-96
; Sequence 96, Application US/08463076E
; Patent No. 5880096
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,076E
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Snyder, Joseph R.
; REGISTRATION NUMBER: 39,381
; REFERENCE/DOCKET NUMBER: 16528A-001850US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-463-076E-96

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  Query Match             28.6%;  Score 28;  DB 2;  Length 12;
  Best Local Similarity   71.4%;  Pred. No. 2.6e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 QPFQVQS 18
              ||: |||
Db          6 QPYSVQS 12


RESULT 28
US-08-463-076E-357
; Sequence 357, Application US/08463076E
; Patent No. 5880096
;  GENERAL INFORMATION:
;    APPLICANT:  Barrett, Ronald W.
;    APPLICANT:  Yanofsky, Stephen D.
;    TITLE OF INVENTION:  Peptides and Compounds That Bind to the
;    TITLE OF INVENTION:  IL-1 Receptor
;    NUMBER OF SEQUENCES:  392
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,076E
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Snyder, Joseph R.
;      REGISTRATION NUMBER:  39,381
;      REFERENCE/DOCKET NUMBER:  16528A-001850US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  357:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  5
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "Xaa = naphthylalanine"
US-08-463-076E-357
```

Query Match 28.6%; Score 28; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy         12 QPFQVQS 18
              ||: |||
Db          6 QPYSVQS 12
```

RESULT 29
US-09-428-082B-673
; Sequence 673, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 673
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-09-428-082B-673

Query Match 28.6%; Score 28; DB 4; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy         12 QPFQVQS 18
              ||: |||
Db          6 QPYSVQS 12
```

RESULT 30
US-09-428-082B-683
; Sequence 683, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371

; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 683
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-09-428-082B-683

  Query Match   28.6%; Score 28; DB 4; Length 12;
  Best Local Similarity   71.4%; Pred. No. 2.6e+02;
  Matches   5; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   12 QPFQVQS 18
              ||: |||
Db   6 QPYSVQS 12

RESULT 31
US-09-428-082B-958
; Sequence 958, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 958
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5)..(5)
;   OTHER INFORMATION: Position 5, Xaa = naphthylalanine
US-09-428-082B-958

  Query Match   28.6%; Score 28; DB 4; Length 12;
  Best Local Similarity   71.4%; Pred. No. 2.6e+02;
  Matches   5; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   12 QPFQVQS 18
              ||: |||
Db   6 QPYSVQS 12

RESULT 32
US-08-347-335A-13
; Sequence 13, Application US/08347335A
; Patent No. 5856163
; GENERAL INFORMATION:
; APPLICANT: Hashida, Miyoko
; APPLICANT: Abo, Masanobu
; APPLICANT: Takamura, Yukiko
; APPLICANT: Kirk, Ole
; APPLICANT: Halkier, Torben
; APPLICANT: Pedersen, Sven
; APPLICANT: Patkar, Shamkant A.
; APPLICANT: Hansen, Mogens T.
; TITLE OF INVENTION: NOVEL ENZYMES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5856163o No. 5856163disk of No. 5856163th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,335A
; FILING DATE: 22-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3706.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-347-335A-13

Query Match 28.6%; Score 28; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          8 KPDLQPF 14
              :||| |:
Db          3 EPDLMPY 9
```

RESULT 33

```
US-08-467-083-53
; Sequence 53, Application US/08467083
; Patent No. 5726023
;  GENERAL INFORMATION:
;    APPLICANT:  Cheever, Martin A.
;    APPLICANT:  Disis, Mary L.
;    TITLE OF INVENTION:  IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
;    TITLE OF INVENTION:  FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH
THE
;    TITLE OF INVENTION:  HER-2/NEU ONCOGENE IS ASSOCIATED
;    NUMBER OF SEQUENCES:  68
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/467,083
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/414,417
;      FILING DATE:  06-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sharkey, Richard G.
;      REGISTRATION NUMBER:  32,629
;      REFERENCE/DOCKET NUMBER:  920010.448C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;      TELEX:  3723836 SEEDANBERRY
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-467-083-53

  Query Match             28.6%;  Score 28;  DB 1;  Length 15;
  Best Local Similarity   45.5%;  Pred. No. 3.3e+02;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 QPPDVEKPDLQ 12
              ||  | :||::
Db          5 QPEYVNQPDVR 15


RESULT 34
US-08-414-417B-53
; Sequence 53, Application US/08414417B
```

; Patent No. 5801005
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH
THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,417B
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-414-417B-53

Query Match 28.6%; Score 28; DB 1; Length 15;
Best Local Similarity 45.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```
Qy          2 QPPDVEKPDLQ 12
              ||  | :||::
Db          5 QPEYVNQPDVR 15
```

RESULT 35
US-08-486-348A-53
; Sequence 53, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

```
;    TITLE OF INVENTION:  FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH
THE
;    TITLE OF INVENTION:  HER-2/neu ONCOGENE IS ASSOCIATED
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/486,348A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sharkey, Richard G.
;      REGISTRATION NUMBER:  32,629
;      REFERENCE/DOCKET NUMBER:  920010.448C6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-486-348A-53

  Query Match             28.6%;  Score 28;  DB 2;  Length 15;
  Best Local Similarity   45.5%;  Pred. No. 3.3e+02;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 QPPDVEKPDLQ 12
              ||  | :||::
Db          5 QPEYVNQPDVR 15


RESULT 36
US-08-468-545B-53
; Sequence 53, Application US/08468545B
; Patent No. 5876712
;  GENERAL INFORMATION:
;    APPLICANT:  Cheever, Martin A.
;    APPLICANT:  Disis, Mary L.
;    TITLE OF INVENTION:  IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;    TITLE OF INVENTION:  FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH
THE
;    TITLE OF INVENTION:  HER-2/neu ONCOGENE IS ASSOCIATED
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
```

```
;       STREET:  6300 Columbia Center, 701 Fifth Avenue
;       CITY:  Seattle
;       STATE:  Washington
;       COUNTRY:  US
;       ZIP:  98104-7092
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/468,545B
;       FILING DATE:  06-JUN-1995
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Sharkey, Richard G.
;       REGISTRATION NUMBER:  32,629
;       REFERENCE/DOCKET NUMBER:  920010.448C5
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206) 622-4900
;       TELEFAX:  (206) 682-6031
;   INFORMATION FOR SEQ ID NO:  53:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  15 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
US-08-468-545B-53

  Query Match             28.6%;  Score 28;  DB 2;  Length 15;
  Best Local Similarity   45.5%;  Pred. No. 3.3e+02;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 QPPDVEKPDLQ 12
              ||  | :||::
Db          5 QPEYVNQPDVR 15


RESULT 37
US-08-466-680B-53
; Sequence 53, Application US/08466680B
; Patent No. 6075122
;  GENERAL INFORMATION:
;     APPLICANT:  Cheever, Martin A.
;     APPLICANT:  Disis, Mary L.
;     TITLE OF INVENTION:  IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;     TITLE OF INVENTION:  FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH
THE
;     TITLE OF INVENTION:  HER-2/neu ONCOGENE IS ASSOCIATED
;     NUMBER OF SEQUENCES:  69
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Seed and Berry LLP
;       STREET:  6300 Columbia Center, 701 Fifth Avenue
;       CITY:  Seattle
;       STATE:  Washington
;       COUNTRY:  US
;       ZIP:  98104-7092
;     COMPUTER READABLE FORM:
```

```
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/466,680B
;       FILING DATE:  06-JUN-1995
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Sharkey, Richard G.
;       REGISTRATION NUMBER:  32,629
;       REFERENCE/DOCKET NUMBER:  920010.448C4
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206) 622-4900
;       TELEFAX:  (206) 682-6031
;   INFORMATION FOR SEQ ID NO:  53:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  15 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
US-08-466-680B-53

  Query Match             28.6%;  Score 28;  DB 3;  Length 15;
  Best Local Similarity   45.5%;  Pred. No. 3.3e+02;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 QPPDVEKPDLQ 12
              ||  | :||::
Db          5 QPEYVNQPDVR 15


RESULT 38
US-09-354-533-53
; Sequence 53, Application US/09354533
; Patent No. 6664370
;   GENERAL INFORMATION:
;        APPLICANT: Cheever, Martin A.
;                   Disis, Mary L.
;        TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;                            FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN
WHICH THE
;                            HER-2/neu ONCOGENE IS ASSOCIATED
;        NUMBER OF SEQUENCES: 69
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Seed and Berry LLP
;             STREET: 6300 Columbia Center, 701 Fifth Avenue
;             CITY: Seattle
;             STATE: Washington
;             COUNTRY: US
;             ZIP: 98104-7092
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/354,533
```

```
;             FILING DATE: 15-Jul-1999
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Sharkey, Richard G.
;             REGISTRATION NUMBER: 32,629
;             REFERENCE/DOCKET NUMBER: 920010.448C9
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 622-4900
;             TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 53:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-354-533-53

  Query Match             28.6%;  Score 28;  DB 4;  Length 15;
  Best Local Similarity   45.5%;  Pred. No. 3.3e+02;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 QPPDVEKPDLQ 12
              ||  | :||::
Db          5 QPEYVNQPDVR 15


RESULT 39
US-08-190-788A-170
; Sequence 170, Application US/08190788A
; Patent No. 5608035
;  GENERAL INFORMATION:
;    APPLICANT:  Yanofsky, Stephen D.
;    APPLICANT:  Barrett, Ronald W.
;    APPLICANT:  Baldwin, David N.
;    APPLICANT:  Jacobs, Jeff W.
;    TITLE OF INVENTION:  Peptides and Compounds That Bind to the
;    TITLE OF INVENTION:  IL-1 Receptor
;    NUMBER OF SEQUENCES:  312
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Affymax Technologies N.V.
;      STREET:  4001 Miranda Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/190,788A
;      FILING DATE:  02-FEB-1994
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/847,567
;      FILING DATE:  05-MAR-1992
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stevens, Lauren L.
;      REGISTRATION NUMBER:  36,691
;      REFERENCE/DOCKET NUMBER:  1019.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-496-2300
;      TELEFAX:  415-424-0832
;  INFORMATION FOR SEQ ID NO:  170:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-190-788A-170

  Query Match             28.6%;  Score 28;  DB 1;  Length 16;
  Best Local Similarity   71.4%;  Pred. No. 3.5e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 QPFQVQS 18
              ||: |||
Db          7 QPYSVQS 13


RESULT 40
US-08-383-474B-173
; Sequence 173, Application US/08383474B
; Patent No. 5767234
;  GENERAL INFORMATION:
;    APPLICANT:  Yanofsky, Stephen D.
;    APPLICANT:  Barrett, Ronald W.
;    APPLICANT:  Baldwin, David N.
;    APPLICANT:  Jacobs, Jeff W.
;    TITLE OF INVENTION:  Peptides and Compounds That Bind to
;    TITLE OF INVENTION:  the IL-1 Receptor
;    NUMBER OF SEQUENCES:  314
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend & Townsend & Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/383,474B
;      FILING DATE:  01-FEB-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/190,788
;      FILING DATE:  02-FEB-1994
;      CLASSIFICATION:  530
```

```
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Stevens, Lauren L.
;       REGISTRATION NUMBER:  36,691
;       REFERENCE/DOCKET NUMBER:  1019.3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-496-2300
;       TELEFAX:  415-424-0832
;   INFORMATION FOR SEQ ID NO:  173:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  16 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-383-474B-173

  Query Match             28.6%;  Score 28;  DB 1;  Length 16;
  Best Local Similarity   71.4%;  Pred. No. 3.5e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 QPFQVQS 18
               ||: |||
Db           7 QPYSVQS 13


RESULT 41
US-08-465-391A-170
; Sequence 170, Application US/08465391A
; Patent No. 5786331
;  GENERAL INFORMATION:
;     APPLICANT:  Barrett, Ronald W.
;     APPLICANT:  Yanofsky, Stephen D.
;     APPLICANT:  Baldwin, David
;     APPLICANT:  Jacobs, Jeff W.
;     APPLICANT:  Bovy, Phillipe R.
;     APPLICANT:  Leahy, Ellen M.
;     APPLICANT:  Pottorf, Richard S.
;     TITLE OF INVENTION:  Peptides and Compounds That Bind to the
;     TITLE OF INVENTION:  IL-1 Receptor
;     NUMBER OF SEQUENCES:  405
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend and Crew
;       STREET:  One Market Plaza, Steuart Tower, Suite 2000
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94105
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/465,391A
;       FILING DATE:  05-JUN-1995
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
```

; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5786331viel, Vern
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-391A-170

Query Match 28.6%; Score 28; DB 1; Length 16;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy         12 QPFQVQS 18
              ||: |||
Db          7 QPYSVQS 13
```

RESULT 42
US-08-464-538B-170
; Sequence 170, Application US/08464538B
; Patent No. 5861476
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Phillipe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/464,538B
;       FILING DATE:  05-JUN-1995
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/373,474
;       FILING DATE:  01-FEB-1995
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/190,788
;       FILING DATE:  02-FEB-1994
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Smith, William M.
;       REGISTRATION NUMBER:  30,223
;       REFERENCE/DOCKET NUMBER:  16528A-001810
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-326-2400
;       TELEFAX:  415-326-2422
;   INFORMATION FOR SEQ ID NO:  170:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  16 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-464-538B-170

  Query Match             28.6%;  Score 28;  DB 2;  Length 16;
  Best Local Similarity   71.4%;  Pred. No. 3.5e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 QPFQVQS 18
              ||: |||
Db          7 QPYSVQS 13


RESULT 43
US-08-463-076E-223
; Sequence 223, Application US/08463076E
; Patent No. 5880096
;  GENERAL INFORMATION:
;     APPLICANT:  Barrett, Ronald W.
;     APPLICANT:  Yanofsky, Stephen D.
;     TITLE OF INVENTION:  Peptides and Compounds That Bind to the
;     TITLE OF INVENTION:  IL-1 Receptor
;     NUMBER OF SEQUENCES:  392
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend and Crew LLP
;       STREET:  Two Embarcadero Center, Eighth Floor
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94111-3834
;     COMPUTER READABLE FORM:
```

```
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/463,076E
;       FILING DATE:  05-JUN-1995
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Snyder, Joseph R.
;       REGISTRATION NUMBER:  39,381
;       REFERENCE/DOCKET NUMBER:  16528A-001850US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 576-0200
;       TELEFAX:  (415) 576-0300
;   INFORMATION FOR SEQ ID NO:  223:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  16 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-463-076E-223

  Query Match             28.6%;  Score 28;  DB 2;  Length 16;
  Best Local Similarity   71.4%;  Pred. No. 3.5e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 QPFQVQS 18
              ||: |||
Db          7 QPYSVQS 13


RESULT 44
US-09-428-082B-786
; Sequence 786, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/09/428,082B
;  CURRENT FILING DATE:  1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 786
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-09-428-082B-786
```

Query Match 28.6%; Score 28; DB 4; Length 16;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy         12 QPFQVQS 18
              ||: |||
Db          7 QPYSVQS 13
```

RESULT 45
US-08-190-788A-169
; Sequence 169, Application US/08190788A
; Patent No. 5608035
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 312
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V.
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,788A
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,567
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-190-788A-169

Query Match 28.6%; Score 28; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy         12 QPFQVQS 18
              ||: |||
Db          8 QPYSVQS 14
```

RESULT 46
US-08-190-788A-230
; Sequence 230, Application US/08190788A
; Patent No. 5608035
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 312
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V.
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,788A
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,567
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 230:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-190-788A-230

Query Match 28.6%; Score 28; DB 1; Length 17;

Best Local Similarity 71.4%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          12 QPFQVQS 18
               ||: |||
Db           8 QPYSVQS 14
```

RESULT 47
US-08-190-788A-233
; Sequence 233, Application US/08190788A
; Patent No. 5608035
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 312
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V.
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,788A
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,567
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 233:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-190-788A-233

Query Match 28.6%; Score 28; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 3.8e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          12 QPFQVQS 18
               ||: |||
Db           8 QPYSVQS 14
```

RESULT 48
US-08-190-788A-234
; Sequence 234, Application US/08190788A
; Patent No. 5608035
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 312
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V.
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,788A
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,567
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 234:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-190-788A-234

Query Match 28.6%; Score 28; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          12 QPFQVQS 18
               ||: |||
Db           8 QPYSVQS 14


RESULT 49
US-08-383-474B-172
; Sequence 172, Application US/08383474B
; Patent No. 5767234
;  GENERAL INFORMATION:
;    APPLICANT:  Yanofsky, Stephen D.
;    APPLICANT:  Barrett, Ronald W.
;    APPLICANT:  Baldwin, David N.
;    APPLICANT:  Jacobs, Jeff W.
;    TITLE OF INVENTION:  Peptides and Compounds That Bind to
;    TITLE OF INVENTION:  the IL-1 Receptor
;    NUMBER OF SEQUENCES:  314
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend & Townsend & Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/383,474B
;      FILING DATE:  01-FEB-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/190,788
;      FILING DATE:  02-FEB-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stevens, Lauren L.
;      REGISTRATION NUMBER:  36,691
;      REFERENCE/DOCKET NUMBER:  1019.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-496-2300
;      TELEFAX:  415-424-0832
;  INFORMATION FOR SEQ ID NO:  172:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-383-474B-172

  Query Match             28.6%;  Score 28;  DB 1;  Length 17;
  Best Local Similarity   71.4%;  Pred. No. 3.8e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          12 QPFQVQS 18
               ||: |||
Db           8 QPYSVQS 14


RESULT 50
US-08-383-474B-233
; Sequence 233, Application US/08383474B
; Patent No. 5767234
;  GENERAL INFORMATION:
;    APPLICANT:  Yanofsky, Stephen D.
;    APPLICANT:  Barrett, Ronald W.
;    APPLICANT:  Baldwin, David N.
;    APPLICANT:  Jacobs, Jeff W.
;    TITLE OF INVENTION:  Peptides and Compounds That Bind to
;    TITLE OF INVENTION:  the IL-1 Receptor
;    NUMBER OF SEQUENCES:  314
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend & Townsend & Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/383,474B
;      FILING DATE:  01-FEB-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/190,788
;      FILING DATE:  02-FEB-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stevens, Lauren L.
;      REGISTRATION NUMBER:  36,691
;      REFERENCE/DOCKET NUMBER:  1019.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-496-2300
;      TELEFAX:  415-424-0832
;  INFORMATION FOR SEQ ID NO:  233:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-383-474B-233

  Query Match           28.6%;  Score 28;  DB 1;  Length 17;
  Best Local Similarity  71.4%;  Pred. No. 3.8e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          12 QPFQVQS 18
                ||: |||
Db           8 QPYSVQS 14
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Search completed: July 4, 2004, 04:48:46
Job time : 12.2836 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:35:16 ; Search time 13.8358 Seconds
(without alignments)
125.142 Million cell updates/sec

Title: US-09-641-802-3
Perfect score: 98
Sequence: 1 DQPPDVEKPDLQPFQVQS 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2898

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	30	30.6	10	2	C35389	urease (EC 3.5.1.5
2	29	29.6	15	2	S20410	protein kinase (EC
3	29	29.6	15	2	PA0041	plastoquinol-plast
4	28.5	29.1	17	2	A42920	fatty acid ethyl e
5	27	27.6	9	2	S66419	tetrameric protein
6	25.5	26.0	17	4	I51887	hypothetical EWSR1
7	25	25.5	15	2	A60221	apolipoprotein A-I
8	24	24.5	10	2	B61218	alpha-gliadin 6Ha
9	24	24.5	14	2	A61362	bradykinin-like pe
10	24	24.5	18	2	PN0149	beta-Gliadine 13 -
11	24	24.5	18	2	A54195	Na+/K+-exchanging
12	23	23.5	9	2	S77984	cytochrome-c oxida
13	23	23.5	11	2	A61365	phyllokinin - Rohd

14	23	23.5	12	2	A61360	vespakinin M - hor
15	23	23.5	12	2	A61359	vespakinin X - hor
16	23	23.5	13	2	G61458	Ig lambda chain V-
17	23	23.5	15	2	PA0088	protein QF200051 -
18	23	23.5	18	2	A60915	enkephalin-degradi
19	22	22.4	12	2	S07436	tachykinin - Afric
20	22	22.4	16	2	JH0517	insulin-like growt
21	21	21.4	11	2	S78765	ribosomal protein
22	21	21.4	12	2	S10059	tachykinin - Afric
23	21	21.4	15	2	PN0665	dystrophin-associa
24	21	21.4	16	2	A60551	leukocyte elastase
25	21	21.4	17	2	B44873	caldesmon - rabbit
26	21	21.4	18	2	S26664	microtubule-associ
27	20	20.4	8	2	I57532	gene TnIslow prote
28	20	20.4	9	2	A61363	bradykinin - commo
29	20	20.4	9	2	D48186	ATPase R1 subunit
30	20	20.4	9	2	S65433	bradykinin - horn
31	20	20.4	9	2	A43065	hydroxyproline-3-b
32	20	20.4	10	2	A60476	S-layer protein -
33	20	20.4	11	2	YHRT	morphogenetic neur
34	20	20.4	11	2	YHHU	morphogenetic neur
35	20	20.4	11	2	YHBO	morphogenetic neur
36	20	20.4	11	2	YHXAE	morphogenetic neur
37	20	20.4	11	2	YHJFHY	morphogenetic neur
38	20	20.4	11	2	S13279	Ile-Ser-bradykinin
39	20	20.4	12	2	C64030	hypothetical prote
40	20	20.4	13	2	S15755	actin 7 - soybean
41	20	20.4	13	2	A61361	bradykinin-like pe
42	20	20.4	15	2	A49155	vasotocin-associat
43	20	20.4	15	2	I49407	placental calcium-
44	20	20.4	15	2	B39109	hypothetical 1.5K
45	20	20.4	15	2	F57789	gallbladder stone
46	20	20.4	17	1	A61339	vespulakinin 1 - e
47	20	20.4	17	2	B61334	trypsin (EC 3.4.21
48	20	20.4	17	2	S15754	actin 6 - soybean
49	20	20.4	17	2	S05033	photosystem II pro
50	20	20.4	17	2	S59481	hydroxyproline-ric
51	20	20.4	18	2	S29166	quinaldine oxidore
52	20	20.4	18	2	A56798	dermatan sulfate p
53	19.5	19.9	11	2	C37196	bradykinin-potenti
54	19.5	19.9	11	2	D37196	bradykinin-potenti
55	19.5	19.9	15	4	I38032	hypothetical MN1/T
56	19	19.4	7	2	S71299	ICL2 protein - Par
57	19	19.4	7	2	PT0283	Ig heavy chain CRD
58	19	19.4	8	2	I48935	apolipoprotein A-I
59	19	19.4	9	2	A61358	bradykinin-like pe
60	19	19.4	9	2	A61057	Thr-6 bradykinin -
61	19	19.4	9	2	A26744	bradykinin-like pe
62	19	19.4	9	2	A60579	bradykinin-like pe
63	19	19.4	9	2	G58502	kidney and bladder
64	19	19.4	10	2	A32543	cardioexcitatory n
65	19	19.4	11	2	B26744	megascoliakinin -
66	19	19.4	11	2	D45900	complement C3b rec
67	19	19.4	12	2	S07206	kassinin - Senegal
68	19	19.4	12	2	T46794	hypothetical prote
69	19	19.4	12	2	S27024	Na+/K+-exchanging
70	19	19.4	12	2	S27023	Na+/K+-exchanging

71	19	19.4	13	2	S21152	tryptophyllin-rela
72	19	19.4	13	2	T08533	hypothetical prote
73	19	19.4	13	2	S22995	hypothetical prote
74	19	19.4	13	2	A33660	osteoclast functio
75	19	19.4	15	2	PS0185	27K protein A 3.4/
76	19	19.4	15	2	PC1313	small granule S6 c
77	19	19.4	15	2	PS0221	gastrin-releasing
78	19	19.4	16	2	D49655	T-cell-receptor be
79	19	19.4	16	2	PH0759	T-cell receptor be
80	19	19.4	17	2	S50901	chlorophyll a/b-bi
81	19	19.4	17	2	S10786	enamelin, 26K - bo
82	19	19.4	17	2	S78421	ribosomal protein
83	18.5	18.9	11	1	XASNBA	bradykinin-potenti
84	18.5	18.9	15	2	S29207	avenin gamma-4 - o
85	18.5	18.9	15	2	PW0004	chlorophyll a/b-bi
86	18	18.4	7	2	I48086	DNA topoisomerase
87	18	18.4	8	2	PT0030	inulinase (EC 3.2.
88	18	18.4	9	2	A61620	locustamyotropin I
89	18	18.4	9	2	B46250	alpha-adaptin - bo
90	18	18.4	10	2	A61007	hementin (EC 3.4.-
91	18	18.4	11	2	PQ0231	beta-glucosidase (
92	18	18.4	11	2	S21127	precorrin methyltr
93	18	18.4	11	2	PS0257	31K protein 3208 -
94	18	18.4	11	2	D56979	collagen alpha 1(I
95	18	18.4	12	2	S36899	ribosomal protein
96	18	18.4	12	2	E44787	calliMIRFamide 1 -
97	18	18.4	12	2	S51737	T-cell receptor be
98	18	18.4	12	2	S71380	lebetin 1 isoform
99	18	18.4	13	2	A05174	tryptophyllin-13 -
100	18	18.4	13	2	I84603	deoxynucleotidyltr

ALIGNMENTS

RESULT 1
C35389
urease (EC 3.5.1.5) 6K chain - Morganella morganii (fragment)
C;Species: Morganella morganii
C;Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 23-Jun-1993
C;Accession: C35389
R;Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.
J. Bacteriol. 172, 3073-3080, 1990
A;Title: Morganella morganii urease: purification, characterization, and
isolation of gene sequences.
A;Reference number: A35389; MUID:90264298; PMID:2345135
A;Accession: C35389
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <HUA>
C;Keywords: hydrolase

Query Match 30.6%; Score 30; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 82;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPDVEK 8

```
              ||:|||
Db          5 PPEVEK 10
```

RESULT 2
S20410
protein kinase (EC 2.7.1.37) - spinach chloroplast (fragment)
N;Alternate names: LHCII protein kinase
C;Species: chloroplast Spinacia oleracea (spinach)
C;Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: S20410
R;Gal, A.; Herrmann, R.G.; Lottspeich, F.; Ohad, I.
FEBS Lett. 298, 33-35, 1992
A;Title: Phosphorylation of cytochrome b6 by the LHC II kinase associated with the cytochrome complex.
A;Reference number: S20410; MUID:92183823; PMID:1544419
A;Accession: S20410
A;Molecule type: protein
A;Residues: 1-15 <GAL>
C;Genetics:
A;Genome: chloroplast
C;Function:
A;Description: is responsible for the regulation of energy distribution between photosystem I and II
A;Note: does not exhibit redox-controlled activation
C;Keywords: chloroplast; light-harvesting complex; membrane-associated complex; phosphotransferase; photosynthesis; thylakoid

```
  Query Match             29.6%;  Score 29;  DB 2;  Length 15;
  Best Local Similarity   75.0%;  Pred. No. 1.9e+02;
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Qy          4 PDVEKPDL 11
              |||||  |
Db          5 PDVEKSTL 12
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RESULT 3
PA0041
plastoquinol-plastocyanin reductase (EC 1.10.99.1) - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 03-Jun-2002
C;Accession: PA0041
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis.
A;Reference number: PA0001
A;Accession: PA0041
A;Molecule type: protein
A;Residues: 1-15 <KAM>
A;Experimental source: leaf
C;Keywords: oxidoreductase

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  Best Local Similarity   62.5%;  Pred. No. 1.9e+02;
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```
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DQPPDVEK 8
              |: ||:||
Db          7 DRVPDMEK 14


RESULT 4
A42920
fatty acid ethyl ester synthase-II - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C;Accession: A42920
R;Bora, P.S.; Wu, X.; Spilburg, C.A.; Lange, L.G.
J. Biol. Chem. 267, 13217-13221, 1992
A;Title: Purification and characterization of fatty acid ethyl ester synthase-II
from human myocardium.
A;Reference number: A42920; MUID:92317032; PMID:1618826
A;Accession: A42920
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-17 <BOR>
A;Experimental source: myocardium
A;Note: sequence extracted from NCBI backbone (NCBIP:107742)

  Query Match             29.1%;  Score 28.5;  DB 2;  Length 17;
  Best Local Similarity   46.2%;  Pred. No. 2.6e+02;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    3;  Gaps    1;

Qy          1 DQPPDVEKPDLQP 13
              : |||   ||  |
Db          1 EDPPD---PDTTP 10


RESULT 5
S66419
tetrameric proteinase precursor, 60K, dithiothreitol-sensitive - spinach
(fragment)
C;Species: Spinacia oleracea (spinach)
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997
C;Accession: S66419
R;Kuwabara, T.
FEBS Lett. 371, 195-198, 1995
A;Title: The 60-kDa precursor to the dithiothreitol-sensitive tetrameric
protease of spinach thylakoids: structural similarities between the protease and
polyphenol oxidase.
A;Reference number: S66419; MUID:95402209; PMID:7672127
A;Accession: S66419
A;Molecule type: protein
A;Residues: 1-9 <KUW>

  Query Match             27.6%;  Score 27;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 PDVEK 8
              |||||
```

```
Db          5 PDVEK 9
```

RESULT 6
I51887
hypothetical EWSR1/FLI1 mutant fusion protein, type 1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
C;Accession: I51887
R;Downing, J.R.; Head, D.R.; Parham, D.M.; Douglass, E.C.; Hulshof, M.G.; Link, M.P.; Motroni, T.A.; Grier, H.E.; Curcio-Brint, A.M.; Shapiro, D.N.
Am. J. Pathol. 143, 1294-1300, 1993
A;Title: Detection of the (11;22)(q24;q12) translocation of Ewing's sarcoma and peripheral neuroectodermal tumor by reverse transcription polymerase chain reaction.
A;Reference number: I51887; MUID:94056652; PMID:8238248
A;Accession: I51887
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-17 <DOW>
A;Cross-references: GB:S66911; NID:g440935; PIDN:AAB28655.1; PID:g440936
C;Comment: This sequence is the chimeric product of a translocation mutation.
C;Genetics:
A;Gene: EWSR1/FLI1; EWS/FLI-1
A;Map position: 22q12/11q24
C;Keywords: fusion protein

  Query Match 26.0%; Score 25.5; DB 4; Length 17;
  Best Local Similarity 46.2%; Pred. No. 7.6e+02;
  Matches 6; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

```
Qy          1 DQPPDVEKPDLQP 13
              |: ||:   || |
Db          7 DEGPDL---DLDP 16
```

RESULT 7
A60221
apolipoprotein A-I - common carp (fragment)
C;Species: Cyprinus carpio (common carp)
C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 31-Dec-1993
C;Accession: A60221
R;Harel, A.; Fainaru, M.; Rubinstein, M.; Tal, N.; Schwartz, M.
J. Neurochem. 55, 1237-1243, 1990
A;Title: Fish apolipoprotein-A-I has heparin binding activity: implication for nerve regeneration.
A;Reference number: A60221; MUID:90376100; PMID:2118944
A;Accession: A60221
A;Molecule type: protein
A;Residues: 1-15 <HAR>
A;Note: protein from plasma and from optic nerve yielded the same sequence
C;Keywords: lipid binding; lipoprotein

  Query Match 25.5%; Score 25; DB 2; Length 15;
  Best Local Similarity 100.0%; Pred. No. 7.9e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 DQPP 4
              ||||
Db          1 DQPP 4
```

RESULT 8
B61218
alpha-gliadin 6Ha - grass (Haynaldia villosa) (fragment)
C;Species: Haynaldia villosa, Dasypyrum villosum
C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 17-Mar-1999
C;Accession: B61218
R;Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafiandra, D.
Biochem. Genet. 29, 207-211, 1991
A;Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynaldia villosa Schur (syn. Dasypyrum villosum L.).
A;Reference number: A61218; MUID:91315394; PMID:1859356
A;Accession: B61218
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SHE>
C;Keywords: seed; storage protein

  Query Match   24.5%; Score 24; DB 2; Length 10;
  Best Local Similarity   62.5%; Pred. No. 7.1e+02;
  Matches   5; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

```
Qy          6 VEKPDLQP 13
              |  | |||
Db          3 VPVPQLQP 10
```

RESULT 9
A61362
bradykinin-like peptide III - Japanese pond frog
C;Species: Rana nigromaculata (Japanese pond frog)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 02-Sep-2000
C;Accession: A61362
R;Nakajima, T.
Chem. Pharm. Bull. 16, 2088-2089, 1968
A;Title: On the third active peptide on smooth muscle in the skin of Rana nigromaculata hallowell.
A;Reference number: A61362; MUID:69117202; PMID:5751736
A;Accession: A61362
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <NAK>
C;Superfamily: unassigned animal peptides
C;Keywords: skin

  Query Match   24.5%; Score 24; DB 2; Length 14;
  Best Local Similarity   50.0%; Pred. No. 1e+03;
  Matches   4; Conservative   1; Mismatches   3; Indels   0; Gaps   0;

```
Qy          9 PDLQPFQV 16
              |   ||:|
Db          3 PGFSPFRV 10
```

RESULT 10
PN0149
beta-Gliadine 13 - Aegilops longissima (fragment)
C;Species: Aegilops longissima
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PN0149
R;Odintsova, T.I.; Egorov, T.A.
Biokhimiia 55, 509-516, 1990
A;Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of polyploid wheat genomes.
A;Reference number: PN0146; MUID:90283493; PMID:2354218
A;Accession: PN0149
A;Molecule type: protein
A;Residues: 1-18 <ODI>
A;Experimental source: strain K-202
C;Superfamily: gliadin

  Query Match   24.5%; Score 24; DB 2; Length 18;
  Best Local Similarity   62.5%; Pred. No. 1.4e+03;
  Matches   5; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   6 VEKPDLQP 13
              | | |||
Db   3 VPVPQLQP 10

RESULT 11
A54195
Na+/K+-exchanging ATPase (EC 3.6.3.9) - spiny dogfish (fragment)
C;Species: Squalus acanthias (spiny dogfish)
C;Date: 13-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 19-Apr-2002
C;Accession: A54195
R;Esmann, M.; Karlish, S.J.; Sottrup-Jensen, L.; Marsh, D.
Biochemistry 33, 8044-8050, 1994
A;Title: Structural integrity of the membrane domains in extensively trypsinized Na,K-ATPase from shark rectal glands.
A;Reference number: A54195; MUID:94297020; PMID:8025109
A;Accession: A54195
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <ESM>
A;Experimental source: rectal gland
A;Note: sequence extracted from NCBI backbone (NCBIP:149363)
C;Keywords: hydrolase

  Query Match   24.5%; Score 24; DB 2; Length 18;
  Best Local Similarity   23.5%; Pred. No. 1.4e+03;
  Matches   4; Conservative   4; Mismatches   9; Indels   0; Gaps   0;

Qy   1 DQPPDVEKPDLQPFQVQ 17
              | | : | |: ::
Db   1 DGPNALTPPPTTPYDIK 17

RESULT 12
S77984

cytochrome-c oxidase (EC 1.9.3.1) chain VIa - bigeye tuna (fragment)
C;Species: Thunnus obesus (bigeye tuna)
C;Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 30-Jan-1998
C;Accession: S77984
R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.
submitted to the Protein Sequence Database, June 1997
A;Reference number: S77980
A;Accession: S77984
A;Molecule type: protein
A;Residues: 1-9 <ARN>
A;Experimental source: heart
C;Genetics:
A;Genome: nuclear
C;Function:
A;Pathway: oxidative phosphorylation; respiratory chain
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane; mitochondrion; oxidative phosphorylation; oxidoreductase; respiratory chain; transmembrane protein

  Query Match 23.5%; Score 23; DB 2; Length 9;
  Best Local Similarity 37.5%; Pred. No. 2.8e+05;
  Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 7 EKPDLQPF 14
      |:|: |:
Db 2 EQPEFVPY 9

RESULT 13
A61365
phyllokinin - Rohde's leaf frog
N;Alternate names: bradykinyl-isoleucyl-tyrosine O-sulfate
C;Species: Phyllomedusa rohdei (Rohde's leaf frog)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000
C;Accession: A61365
R;Anastasi, A.; Bertaccini, G.; Erspamer, V.
Br. J. Pharmacol. 27, 479-485, 1966
A;Title: Pharmacological data on phyllokinin (bradykinyl-isoleucyl-tyrosine O-sulphate) and bradykinyl-isoleucyl-tyrosine.
A;Reference number: A61365; MUID:67179312; PMID:5970899
A;Accession: A61365
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <ANA>
C;Superfamily: unassigned animal peptides
C;Keywords: sulfoprotein
F;11/Binding site: sulfate (Tyr) (covalent) #status experimental

  Query Match 23.5%; Score 23; DB 2; Length 11;
  Best Local Similarity 37.5%; Pred. No. 1.1e+03;
  Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQV 16
      | ||::
Db 3 PGFSPFRI 10

RESULT 14
A61360
vespakinin M - hornet (Vespa mandarinia)
C;Species: Vespa mandarinia
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000
C;Accession: A61360
R;Kishimura, H.; Yasuhara, T.; Yoshida, H.; Nakajima, T.
Chem. Pharm. Bull. 24, 2896-2897, 1976
A;Title: Vespakinin-M, a novel bradykinin analogue containing hydroxyproline, in the venom of Vespa mandarinia Smith.
A;Reference number: A61360; MUID:77114342; PMID:1017116
A;Accession: A61360
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <KIS>
C;Superfamily: unassigned animal peptides
C;Keywords: hydroxyproline; venom
F;4/Modified site: 4-hydroxyproline (Pro) #status experimental

  Query Match   23.5%; Score 23; DB 2; Length 12;
  Best Local Similarity   37.5%; Pred. No. 1.3e+03;
  Matches   3; Conservative   2; Mismatches   3; Indels   0; Gaps   0;

Qy   9 PDLQPFQV 16
              | ||::
Db   4 PGFSPFRI 11

RESULT 15
A61359
vespakinin X - hornet (Vespa xanthoptera)
C;Species: Vespa xanthoptera
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000
C;Accession: A61359
R;Yasuhara, T.; Yoshida, H.; Nakajima, T.
Chem. Pharm. Bull. 25, 936-941, 1977
A;Title: Chemical investigation of the hornet (Vespa xanthoptera Cameron) venom. The structure of a new bradykinin analogue vespakinin-X.
A;Reference number: A61359; MUID:87187853; PMID:264186
A;Accession: A61359
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <YAS>
C;Superfamily: unassigned animal peptides
C;Keywords: venom

  Query Match   23.5%; Score 23; DB 2; Length 12;
  Best Local Similarity   37.5%; Pred. No. 1.3e+03;
  Matches   3; Conservative   2; Mismatches   3; Indels   0; Gaps   0;

Qy   9 PDLQPFQV 16
              | ||::
Db   4 PGFSPFRI 11

RESULT 16

G61458
Ig lambda chain V-II region (AZI) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C;Accession: G61458; PL0159
R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A;Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-associated glycoprotein and characterization of the variability subgroup of their heavy and light chains.
A;Reference number: A61458; MUID:90039128; PMID:2478651
A;Accession: G61458
A;Molecule type: protein
A;Residues: 1-13 <BRO>
C;Comment: This protein is one of monoclonal IgM reactive with myelin-associated glycoprotein.
C;Keywords: heterotetramer; immunoglobulin

  Query Match 23.5%; Score 23; DB 2; Length 13;
  Best Local Similarity 80.0%; Pred. No. 1.4e+03;
  Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QPPDV 6
      ||| |
Db 6 QPPSV 10

RESULT 17
PA0088
protein QF200051 - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0088
R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A;Description: Two dimensional polyacrylamide gel electropheresis of Fusarium sporotrichisides proteins.
A;Reference number: PA0051
A;Accession: PA0088
A;Molecule type: protein
A;Residues: 1-15 <CHO>

  Query Match 23.5%; Score 23; DB 2; Length 15;
  Best Local Similarity 44.4%; Pred. No. 1.6e+03;
  Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 QPPDVEKPD 10
      | ||: |
Db 1 QKPDIPXDD 9

RESULT 18
A60915
enkephalin-degrading aminopeptidase (EC 3.4.-.-), puromycin-sensitive - rat (fragment)
N;Alternate names: aminoenkephalinase; aminopeptidase MII

C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jan-2000
C;Accession: A60915
R;Dyer, S.H.; Slaughter, C.A.; Orth, K.; Moomaw, C.R.; Hersh, L.B.
J. Neurochem. 54, 547-554, 1990
A;Title: Comparison of the soluble and membrane-bound forms of the puromycin-sensitive enkephalin-degrading aminopeptidases from rat.
A;Reference number: A60915; MUID:90132681; PMID:2299352
A;Accession: A60915
A;Molecule type: protein
A;Residues: 1-18 <DYE>
A;Note: this sequence represents the N-terminus of both soluble and membrane-associated forms
C;Superfamily: membrane alanyl aminopeptidase
C;Keywords: hydrolase

  Query Match   23.5%; Score 23; DB 2; Length 18;
  Best Local Similarity   42.9%; Pred. No. 2e+03;
  Matches   3; Conservative   3; Mismatches   1; Indels   0; Gaps   0;

Qy   9 PDLQPFQ 15
              |: :||:
Db   1 PEKRPFE 7

RESULT 19
S07436
tachykinin - African tree frog (Kassina maculata)
N;Alternate names: hylambatin
C;Species: Kassina maculata
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Sep-2000
C;Accession: S07436
R;Yasuhara, T.; Nakajima, T.; Erspamer, G.F.; Erspamer, V.
Biomed. Res. 2, 613-617, 1981
A;Title: New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and hylambatin, in the skin of the African rhacophorid frog Hylambates maculatus.
A;Reference number: S07436
A;Accession: S07436
A;Molecule type: protein
A;Residues: 1-12 <YAS>
A;Experimental source: skin
A;Note: the source is designated as Hylambates maculatus
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
F;12/Modified site: amidated carboxyl end (Met) #status predicted

  Query Match   22.4%; Score 22; DB 2; Length 12;
  Best Local Similarity   50.0%; Pred. No. 1.8e+03;
  Matches   3; Conservative   2; Mismatches   1; Indels   0; Gaps   0;

Qy   3 PPDVEK 8
              ||| ::
Db   2 PPDPDR 7

RESULT 20
JH0517

insulin-like growth factor-binding protein 4 - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 03-Nov-2003
C;Accession: JH0517
R;Coleman, M.E.; Pan, Y.C.E.; Etherton, T.D.
Biochem. Biophys. Res. Commun. 181, 1131-1136, 1991
A;Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth factor-binding proteins in porcine serum.
A;Reference number: JH0515; MUID:92109718; PMID:1722398
A;Accession: JH0517
A;Molecule type: protein
A;Residues: 1-16 <COL>
A;Experimental source: serum
C;Superfamily: insulin-like growth factor binding protein; thyroglobulin type I repeat homology

  Query Match   22.4%; Score 22; DB 2; Length 16;
  Best Local Similarity   66.7%; Pred. No. 2.5e+03;
  Matches   4; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   3 PPDVEK 8
              || ||
Db   8 PPSEEK 13

RESULT 21
S78765
ribosomal protein MRP-S24, mitochondrial - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: S78765
R;Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A;Reference number: S78760
A;Accession: S78765
A;Molecule type: protein
A;Residues: 1-11 <GRA>
C;Keywords: mitochondrion
F;1-11/Product: ribosomal protein MRP-S24 (fragment) #status experimental <MAT>

  Query Match   21.4%; Score 21; DB 2; Length 11;
  Best Local Similarity   50.0%; Pred. No. 2.3e+03;
  Matches   4; Conservative   1; Mismatches   3; Indels   0; Gaps   0;

Qy   1 DQPPDVEK 8
              | | |: |
Db   4 DVPKDLTK 11

RESULT 22
S10059
tachykinin - African tree frog (Kassina maculata)
N;Alternate names: hylambates-kassinin
C;Species: Kassina maculata
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Sep-2000
C;Accession: S10059
R;Yasuhara, T.; Nakajima, T.; Erspamer, G.F.; Erspamer, V.

Biomed. Res. 2, 613-617, 1981
A;Title: New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and hylambatin, in the skin of the African rhacophorid frog Hylambates maculatus.
A;Reference number: S07436
A;Accession: S10059
A;Molecule type: protein
A;Residues: 1-12 <YAS>
A;Experimental source: skin
A;Note: the source is designated as Hylambates maculatus
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
F;12/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 21.4%; Score 21; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          5 DVEKPD 10
              |  |||
Db          1 DEPKPD 6
```

RESULT 23
PN0665
dystrophin-associated glycoprotein A3a-IV - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
C;Accession: PN0665
R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
J. Biochem. 114, 634-639, 1993
A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained in Duchenne muscular dystrophy muscle.
A;Reference number: PN0662; MUID:94156881; PMID:8113213
A;Accession: PN0665
A;Molecule type: protein
A;Residues: 1-15 <YOS>
C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
C;Keywords: glycoprotein; skeletal muscle

Query Match 21.4%; Score 21; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 3.3e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy          9 PDLQPFQ 15
              |:  |:|
Db          9 PNAPPYQ 15
```

RESULT 24
A60551
leukocyte elastase (EC 3.4.21.37) - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 17-Mar-1999
C;Accession: A60551
R;Axelsson, L.; Bergenfeldt, M.; Bjoerk, P.; Olsson, R.; Ohlsson, K.
Scand. J. Clin. Lab. Invest. 50, 35-42, 1990

A;Title: Release of immunoreactive canine leukocyte elastase normally and in endotoxin and pancreatitic shock.
A;Reference number: A60551; MUID:90193608; PMID:1690443
A;Accession: A60551
A;Molecule type: protein
A;Residues: 1-16 <AXE>
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; leukocyte; lysosome; serine proteinase

Query Match 21.4%; Score 21; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 3.6e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```
Qy          8 KPDLQPFQV 16
              :|   || |
Db          8 QPHAWPFMV 16
```

RESULT 25
B44873
caldesmon - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 04-Mar-2000
C;Accession: B44873
R;Ikebe, M.; Hornick, T.
Arch. Biochem. Biophys. 288, 538-542, 1991
A;Title: Determination of the phosphorylation sites of smooth muscle caldesmon by protein kinase C.
A;Reference number: A44873; MUID:91378498; PMID:1898046
A;Accession: B44873
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <IKE>
A;Experimental source: skeletal myosin
A;Note: sequence extracted from NCBI backbone (NCBIP:63202)
C;Superfamily: caldesmon

Query Match 21.4%; Score 21; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          6 VEKP 9
              ||||
Db          8 VEKP 11
```

RESULT 26
S26664
microtubule-associated protein tau - human
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995
C;Accession: S26664
R;Andreadis, A.; Brown, W.M.; Kosik, K.S.
Biochemistry 31, 10626-10633, 1992
A;Title: Structure and novel exons of the human tau gene.
A;Reference number: S26662; MUID:93041757; PMID:1420178
A;Accession: S26664

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-18 <AND>
A;Cross-references: EMBL:X61375
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991

  Query Match 21.4%; Score 21; DB 2; Length 18;
  Best Local Similarity 41.7%; Pred. No. 4.1e+03;
  Matches 5; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

```
Qy          1 DQPPDVEKPDLQ 12
              |. |  :: |||:
Db          8 DHP--LQGPDLR 17
```

RESULT 27
I57532
gene TnIslow protein - rat (fragment)
C;Species: Rattus sp. (rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Feb-1997
C;Accession: I57532
R;Banerjee-Basu, S.; Buonanno, A.
Mol. Cell. Biol. 13, 7019-7028, 1993
A;Title: cis-acting sequences of the rat troponin I slow gene confer tissue- and development-specific transcription in cultured muscle cells as well as fiber type specificity in transgenic mice.
A;Reference number: I57532; MUID:94019373; PMID:8413291
A;Accession: I57532
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-8 <RES>
A;Cross-references: GB:S66172; NID:g432603
C;Genetics:
A;Gene: TnIslow

  Query Match 20.4%; Score 20; DB 2; Length 8;
  Best Local Similarity 60.0%; Pred. No. 2.8e+05;
  Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 PDVEK 8
              |:||:
Db          2 PEVER 6
```

RESULT 28
A61363
bradykinin - common frog
C;Species: Rana temporaria (common frog)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000
C;Accession: A61363
R;Anastasi, A.; Erspamer, V.; Bertaccini, G.
Comp. Biochem. Physiol. A 14, 43-52, 1965
A;Title: Occurrence of bradykinin in the skin of Rana temporaria.
A;Reference number: A61363
A;Accession: A61363
A;Status: preliminary

A;Molecule type: protein
A;Residues: 1-9 <ANA>
C;Superfamily: unassigned animal peptides
C;Keywords: skin

  Query Match 20.4%; Score 20; DB 2; Length 9;
  Best Local Similarity 42.9%; Pred. No. 2.8e+05;
  Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy          9 PDLQPFQ 15
              |   ||:
Db          3 PGFSPFR 9
```

RESULT 29
D48186
ATPase R1 subunit - wood tobacco (fragment)
C;Species: Nicotiana sylvestris (wood tobacco)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 23-Feb-1997
C;Accession: D48186
R;De Paepe, R.; Forchioni, A.; Chetrit, P.; Vedel, F.
Proc. Natl. Acad. Sci. U.S.A. 90, 5934-5938, 1993
A;Title: Specific mitochondrial proteins in pollen: presence of an additional ATP synthase beta subunit.
A;Reference number: A48186; MUID:93317598; PMID:8327463
A;Accession: D48186
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <DE1>
A;Experimental source: pollen
A;Note: sequence extracted from NCBI backbone (NCBIP:134871)

  Query Match 20.4%; Score 20; DB 2; Length 9;
  Best Local Similarity 50.0%; Pred. No. 2.8e+05;
  Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy         10 DLQPFQ 15
              || |::
Db          4 DLAPYK 9
```

RESULT 30
S65433
bradykinin - horn fly (fragment)
C;Species: Haematobia irritans (horn fly)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S65433
R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen, P.
Eur. J. Biochem. 237, 414-423, 1996
A;Title: Cloning and characterisation of angiotensin-converting enzyme from the dipteran species, Haematobia irritans exigua, and its expression in the maturing male reproductive system.
A;Reference number: S65431; MUID:96215437; PMID:8647080
A;Accession: S65433
A;Status: preliminary
A;Molecule type: protein

A;Residues: 1-9 <WIJ>
A;Note: the source is designated as Haematobia irritans exigua

  Query Match 20.4%; Score 20; DB 2; Length 9;
  Best Local Similarity 42.9%; Pred. No. 2.8e+05;
  Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQ 15
      | ||:
Db 3 PGFSPFR 9

RESULT 31
A43065
hydroxyproline-3-bradykinin - frog (Heleophryne purcelli)
C;Species: Heleophryne purcelli
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C;Accession: A43065
R;Nakajima, T.; Yasuhara, T.; Erspamer, G.F.; Visser, J.
Experientia 35, 1133, 1979
A;Title: Occurrence of Hyp(3)-bradykinin in methanol extracts of the skin of the South African leptodactylid frog Heleophryne purcelli.
A;Reference number: A43065; MUID:80024576; PMID:488255
A;Accession: A43065
A;Molecule type: protein
A;Residues: 1-9 <NAK>
C;Keywords: bradykinin; hydroxyproline; skin
F;3/Modified site: hydroxyproline (Pro) #status experimental

  Query Match 20.4%; Score 20; DB 2; Length 9;
  Best Local Similarity 42.9%; Pred. No. 2.8e+05;
  Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQ 15
      | ||:
Db 3 PGFSPFR 9

RESULT 32
A60476
S-layer protein - Bacillus thuringiensis (fragment)
C;Species: Bacillus thuringiensis
C;Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 12-Mar-1993
C;Accession: A60476
R;Luckevich, M.D.; Beveridge, T.J.
J. Bacteriol. 171, 6656-6667, 1989
A;Title: Characterization of a dynamic S layer on Bacillus thuringiensis.
A;Reference number: A60476; MUID:90078111; PMID:2592346
A;Accession: A60476
A;Molecule type: protein
A;Residues: 1-10 <LUC>
C;Comment: The S-layer, or surface array, is the outermost component of several archaebacteria and eubacteria.

  Query Match 20.4%; Score 20; DB 2; Length 10;
  Best Local Similarity 60.0%; Pred. No. 3e+03;
  Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          9 PDLQP 13
              ||: |
Db          6 PDVXP 10
```

RESULT 33
YHRT
morphogenetic neuropeptide - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C;Accession: A01427
R;Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981
A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.
A;Reference number: A93266; MUID:82035850; PMID:7290191
A;Accession: A01427
A;Molecule type: protein
A;Residues: 1-11 <BOD>
R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A;Title: Synthesis of a new neuropeptide, the head activator from hydra.
A;Reference number: A91296; MUID:82050803; PMID:7297679
A;Contents: annotation; synthesis
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator by the authors, because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.
C;Superfamily: unassigned animal peptides
C;Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

```
  Query Match             20.4%;  Score 20;  DB 2;  Length 11;
  Best Local Similarity   57.1%;  Pred. No. 3.3e+03;
  Matches    4;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 QPPDVEK 8
              |||   |
Db          1 QPPGGSK 7
```

RESULT 34
YHHU
morphogenetic neuropeptide - human
C;Species: Homo sapiens (man)
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C;Accession: B01427; A01427
R;Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981
A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.
A;Reference number: A93266; MUID:82035850; PMID:7290191
A;Accession: B01427

A;Molecule type: protein
A;Residues: 1-11 <BOD>
R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A;Title: Synthesis of a new neuropeptide, the head activator from hydra.
A;Reference number: A91296; MUID:82050803; PMID:7297679
A;Contents: annotation; synthesis
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.
C;Superfamily: unassigned animal peptides
C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide
F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 20.4%; Score 20; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          2 QPPDVEK 8
              |||   |
Db          1 QPPGGSK 7
```

RESULT 35
YHBO
morphogenetic neuropeptide - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C;Accession: C01427; A01427
R;Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981
A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.
A;Reference number: A93266; MUID:82035850; PMID:7290191
A;Accession: C01427
A;Molecule type: protein
A;Residues: 1-11 <BOD>
R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A;Title: Synthesis of a new neuropeptide, the head activator from hydra.
A;Reference number: A91296; MUID:82050803; PMID:7297679
A;Contents: annotation; synthesis
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.
C;Superfamily: unassigned animal peptides
C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide

F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

```
  Query Match             20.4%;  Score 20;  DB 2;  Length 11;
  Best Local Similarity   57.1%;  Pred. No. 3.3e+03;
  Matches    4;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 QPPDVEK 8
              |||   |
Db          1 QPPGGSK 7
```

RESULT 36
YHXAE
morphogenetic neuropeptide - sea anemone (Anthopleura elegantissima)
N;Alternate names: head activator
C;Species: Anthopleura elegantissima
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C;Accession: A93900; A01427
R;Schaller, H.C.; Bodenmuller, H.
Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981
A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.
A;Reference number: A93900
A;Accession: A93900
A;Molecule type: protein
A;Residues: 1-11 <SCH>
R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A;Title: Synthesis of a new neuropeptide, the head activator from hydra.
A;Reference number: A91296; MUID:82050803; PMID:7297679
A;Contents: annotation; synthesis
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.
C;Superfamily: unassigned animal peptides
C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

```
  Query Match             20.4%;  Score 20;  DB 2;  Length 11;
  Best Local Similarity   57.1%;  Pred. No. 3.3e+03;
  Matches    4;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 QPPDVEK 8
              |||   |
Db          1 QPPGGSK 7
```

RESULT 37
YHJFHY
morphogenetic neuropeptide - Hydra attenuata
N;Alternate names: head activator
C;Species: Hydra attenuata
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: B93900; A01427
R;Schaller, H.C.; Bodenmuller, H.
Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981
A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.
A;Reference number: A93900
A;Accession: B93900
A;Molecule type: protein
A;Residues: 1-11 <SCH>
R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A;Title: Synthesis of a new neuropeptide, the head activator from hydra.
A;Reference number: A91296; MUID:82050803; PMID:7297679
A;Contents: annotation; synthesis
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.
C;Superfamily: unassigned animal peptides
C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

  Query Match 20.4%; Score 20; DB 2; Length 11;
  Best Local Similarity 57.1%; Pred. No. 3.3e+03;
  Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QPPDVEK 8
      ||| |
Db 1 QPPGGSK 7

RESULT 38
S13279
Ile-Ser-bradykinin - human (fragment)
N;Alternate names: T-kinin
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 24-Jul-1998
C;Accession: S13279
R;Wunderer, G.; Walter, I.; Eschenbacher, B.; Lang, M.; Kellermann, J.; Kindermann, G.
Biol. Chem. Hoppe-Seyler 371, 977-981, 1990
A;Title: Ile-Ser-bradykinin is an aberrant permeability factor in various human malignant effusions.
A;Reference number: S13279; MUID:91166748; PMID:2076202
A;Accession: S13279
A;Molecule type: protein
A;Residues: 1-11 <WUN>
C;Keywords: bradykinin

  Query Match 20.4%; Score 20; DB 2; Length 11;
  Best Local Similarity 42.9%; Pred. No. 3.3e+03;
  Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQ 15
      | ||:

```
Db          5 PGFSPFR 11
```

RESULT 39
C64030
hypothetical protein HI1451 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 10-Oct-1997
C;Accession: C64030
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.; Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.; FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: C64030
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-12 <TIGR>
A;Cross-references: GB:U32823; GB:L42023; NID:g1574281; PID:g1574296; TIGR:HI1451

```
  Query Match             20.4%;  Score 20;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 PPD 5
              |||
Db          9 PPD 11
```

RESULT 40
S15755
actin 7 - soybean (fragment)
C;Species: Glycine max (soybean)
C;Date: 20-Feb-1995 #sequence_revision 29-May-1998 #text_change 13-Aug-1999
C;Accession: S15755
R;Pearson, L.; Meagher, R.B.
Plant Mol. Biol. 14, 513-526, 1990
A;Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated leader: structural similarity to vertebrate muscle actin genes.
A;Reference number: S15754; MUID:91346640; PMID:2102831
A;Accession: S15755
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-13 <PEA>
A;Cross-references: EMBL:X17120; NID:g18527; PIDN:CAA34980.1; PID:g18528
C;Superfamily: actin
C;Keywords: cytoskeleton; structural protein

Query Match 20.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy         10 DLQP 13
                |:||
Db          6 DIQP 9
```

RESULT 41
A61361
bradykinin-like peptide - Bombina orientalis
C;Species: Bombina orientalis
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000
C;Accession: A61361
R;Yasuhara, T.; Hira, M.; Nakajima, T.; Yanaihara, N.; Yanaihara, C.; Hashimoto, T.; Sakura, N.; Tachibana, S.; Araki, K.; Bessho, M.; Yamanaka, T.
Chem. Pharm. Bull. 21, 1388-1391, 1973
A;Title: Active peptides on smooth muscle in the skin of Bombina orientalis Boulenger and characterization of a new bradykinin analogue.
A;Reference number: A61361; MUID:73256822; PMID:4732297
A;Accession: A61361
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <YAS>
C;Superfamily: unassigned animal peptides
C;Keywords: skin

Query Match 20.4%; Score 20; DB 2; Length 13;
Best Local Similarity 42.9%; Pred. No. 4e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy          9 PDLQPFQ 15
                |   ||:
Db          3 PGFSPFR 9
```

RESULT 42
A49155
vasotocin-associated neurophysin - African toad (fragment)
N;Alternate names: MSEL-neurophysin
C;Species: Bufo regularis (African toad)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2001
C;Accession: A49155
R;Chauvet, J.; Ouedraogo, Y.; Michel, G.; Acher, R.
Comp. Biochem. Physiol. Comp. Physiol. 104, 497-502, 1993
A;Title: Vasotocin and hydrin 2 (vasotocinyl-Gly) in the African toad Bufo regularis: study under various environmental conditions.
A;Reference number: A49155; MUID:93230882; PMID:8097151
A;Accession: A49155
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <CHA>
A;Note: sequence extracted from NCBI backbone (NCBIP:129814)
C;Superfamily: oxytocin-neurophysin
C;Keywords: neuropeptide

Query Match 20.4%; Score 20; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          4 PDVEKPDLQP 13
              ||   |   |
Db          3 PDTAVPQCIP 12
```

RESULT 43
I49407
placental calcium-binding protein - western wild mouse (fragment)
C;Species: Mus spretus (western wild mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C;Accession: I49407
R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A;Reference number: I48934; MUID:94319082; PMID:8043949
A;Accession: I49407
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-15 <RES>
A;Cross-references: EMBL:U05696; NID:g497016; PIDN:AAA61936.1; PID:g497017
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: calcium binding; EF hand

Query Match 20.4%; Score 20; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          9 PDLQP 13
              || :|
Db          8 PDKEP 12
```

RESULT 44
B39109
hypothetical 1.5K protein - hepatitis C virus
N;Alternate names: hypothetical protein 2
C;Species: hepatitis C virus
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999
C;Accession: B39109; JQ1585
R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-Olson, P.; Kuo, G.; Choo, Q.L.; Houghton, M.
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
A;Title: Characterization of the terminal regions of hepatitis C viral RNA: identification of conserved sequences in the 5' untranslated region and poly(A) tails at the 3' end.
A;Reference number: A39109; MUID:91156678; PMID:1705704
A;Accession: B39109
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-15 <HAN>
A;Cross-references: GB:M58406
R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.

J. Gen. Virol. 73, 1521-1525, 1992
A;Title: Cloning and sequencing of the structural region and expression of putative core gene of hepatitis C virus from a British case of chronic sporadic hepatitis.
A;Reference number: JQ1584; MUID:92300349; PMID:1318944
A;Accession: JQ1585
A;Molecule type: genomic RNA
A;Residues: 1-15 <KUM>
A;Experimental source: strain U.K.

  Query Match 20.4%; Score 20; DB 2; Length 15;
  Best Local Similarity 50.0%; Pred. No. 4.7e+03;
  Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9
      ||| |
Db 5 QPPGPPLP 12

RESULT 45
F57789
gallbladder stone matrix protein 2, 41K - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 03-May-1996
C;Accession: F57789
R;Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, February 1996
A;Description: The proteins of gallbladder stones.
A;Reference number: A57789
A;Accession: F57789
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <BIN>
A;Note: 9-Phe was also found

  Query Match 20.4%; Score 20; DB 2; Length 15;
  Best Local Similarity 75.0%; Pred. No. 4.7e+03;
  Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 EKPD 10
      :|||
Db 3 DKPD 6

RESULT 46
A61339
vespulakinin 1 - eastern yellowjacket
N;Contains: vespulakinin 2
C;Species: Vespula maculifrons (eastern yellowjacket)
C;Date: 17-Jul-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C;Accession: A61339
R;Yoshida, H.; Geller, R.G.; Pisano, J.J.
Biochemistry 15, 61-64, 1976
A;Title: Vespulakinins: new carbohydrate-containing bradykinin derivatives.
A;Reference number: A61339; MUID:76114777; PMID:1247511
A;Accession: A61339
A;Molecule type: protein

A;Residues: 1-17 <YOS>
C;Superfamily: vespulakinin
C;Keywords: antihypertensive; bradykinin; glycoprotein; venom
F;1-17/Product: vespulakinin 1 #status experimental <MAT1>
F;3-17/Product: vespulakinin 2 #status experimental <MAT2>
F;9-17/Region: bradykinin-like
F;3,4/Binding site: carbohydrate (Thr) (covalent) #status experimental

  Query Match 20.4%; Score 20; DB 1; Length 17;
  Best Local Similarity 42.9%; Pred. No. 5.4e+03;
  Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy          9 PDLQPFQ 15
              |   ||:
Db         11 PGFSPFR 17
```

RESULT 47
B61334
trypsin (EC 3.4.21.4) 2 - starfish (Dermasterias imbricata) (fragment)
C;Species: Dermasterias imbricata
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
C;Accession: B61334
R;Estell, D.A.; Laskowski Jr., M.
Biochemistry 19, 124-131, 1980
A;Title: Dermasterias imbricata trypsin 1: an enzyme which rapidly hydrolyzes the reactive-site peptide bonds of protein trypsin inhibitors.
A;Reference number: A61334; MUID:80109692; PMID:7352972
A;Accession: B61334
A;Molecule type: protein
A;Residues: 1-17 <EST>
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase

  Query Match 20.4%; Score 20; DB 2; Length 17;
  Best Local Similarity 60.0%; Pred. No. 5.4e+03;
  Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy         12 QPFQV 16
              :|:||
Db         12 RPYQV 16
```

RESULT 48
S15754
actin 6 - soybean (fragment)
C;Species: Glycine max (soybean)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 13-Aug-1999
C;Accession: S15754; S08049
R;Pearson, L.; Meagher, R.B.
Plant Mol. Biol. 14, 513-526, 1990
A;Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated leader: structural similarity to vertebrate muscle actin genes.
A;Reference number: S15754; MUID:91346640; PMID:2102831
A;Accession: S15754
A;Molecule type: DNA
A;Residues: 1-17 <PEA>

A;Cross-references: EMBL:X17119; NID:g18525; PIDN:CAA34979.1; PID:g18526
C;Superfamily: actin
C;Keywords: cytoskeleton

  Query Match 20.4%; Score 20; DB 2; Length 17;
  Best Local Similarity 75.0%; Pred. No. 5.4e+03;
  Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
       |:||
Db 6 DIQP 9

RESULT 49
S05033
photosystem II protein psbL - Synechococcus sp. (strain Copeland) (fragment)
N;Alternate names: photosystem II 5K protein
C;Species: Synechococcus sp.
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
C;Accession: S05033
R;Ikeuchi, M.; Koike, H.; Inoue, Y.
FEBS Lett. 251, 155-160, 1989
A;Title: Identification of psbI and psbL gene products in cyanobacterial
photosystem II reaction center preparation.
A;Reference number: S05030
A;Accession: S05033
A;Molecule type: protein
A;Residues: 1-17 <IKE>
A;Note: the source is designated as Synechococcus vulcanus
C;Genetics:
A;Gene: psbL
C;Keywords: photosynthesis; photosystem II; thylakoid

  Query Match 20.4%; Score 20; DB 2; Length 17;
  Best Local Similarity 37.5%; Pred. No. 5.4e+03;
  Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 9 PDLQPFQV 16
      |: || ::
Db 5 PNRQPVEL 12

RESULT 50
S59481
hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)
C;Species: Phaseolus vulgaris (kidney bean)
C;Date: 27-Apr-1996 #sequence_revision 19-Jul-1996 #text_change 05-Dec-1998
C;Accession: S59481
R;Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.
Plant Mol. Biol. 28, 1075-1087, 1995
A;Title: Specificity in the immobilisation of cell wall proteins in response to
different elicitor molecules in suspension-cultured cells of French bean
(Phaseolus vulgaris L.).
A;Reference number: S59481; MUID:96011753; PMID:7548825
A;Accession: S59481
A;Molecule type: protein
A;Residues: 1-17 <WOJ>

C;Keywords: glycoprotein; hydroxyproline
F;6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 20.4%; Score 20; DB 2; Length 17;
Best Local Similarity 57.1%; Pred. No. 5.4e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          3 PPDVEKP 9
              || |  |
Db          9 PPPVVYP 15
```

Search completed: July 4, 2004, 04:47:15
Job time : 14.8358 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:45:52 ; Search time 35.3284 Seconds
(without alignments)
158.601 Million cell updates/sec

Title: US-09-641-802-3
Perfect score: 98
Sequence: 1 DQPPDVEKPDLQPFQVQS 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 203405

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	98	100.0	18	14	US-10-281-652-3	Sequence 3, Appli
2	41	41.8	15	12	US-10-014-340-759	Sequence 759, App
3	39	39.8	16	14	US-10-225-567A-1755	Sequence 1755, Ap
4	35	35.7	12	12	US-10-014-340-526	Sequence 526, App
5	32	32.7	9	14	US-10-350-258-6	Sequence 6, Appli
6	32	32.7	18	14	US-10-161-791-305	Sequence 305, App
7	31	31.6	10	10	US-09-572-404B-3283	Sequence 3283, Ap
8	31	31.6	11	12	US-10-601-837-34	Sequence 34, Appl
9	30	30.6	11	14	US-10-022-066-144	Sequence 144, App
10	30	30.6	11	14	US-10-022-066-374	Sequence 374, App
11	30	30.6	15	15	US-10-149-138-3845	Sequence 3845, Ap
12	30	30.6	15	16	US-10-149-138-3845	Sequence 3845, Ap
13	29	29.6	8	12	US-09-891-823-98	Sequence 98, Appl
14	29	29.6	8	14	US-10-365-908-98	Sequence 98, Appl
15	29	29.6	9	14	US-10-033-662-36	Sequence 36, Appl
16	29	29.6	10	10	US-09-572-404B-3027	Sequence 3027, Ap
17	29	29.6	13	10	US-09-992-665-47	Sequence 47, Appl
18	29	29.6	15	14	US-10-080-608A-70	Sequence 70, Appl
19	29	29.6	15	15	US-10-370-685-159	Sequence 159, App
20	29	29.6	15	15	US-10-371-067-1	Sequence 1, Appli
21	29	29.6	17	14	US-10-225-567A-1370	Sequence 1370, Ap
22	29	29.6	17	16	US-10-443-349-12	Sequence 12, Appl
23	29	29.6	18	9	US-09-922-261-200	Sequence 200, App
24	28	28.6	9	15	US-10-107-532-25	Sequence 25, Appl
25	28	28.6	9	15	US-10-107-532-652	Sequence 652, App
26	28	28.6	9	15	US-10-107-532-2214	Sequence 2214, Ap
27	28	28.6	9	15	US-10-107-532-2776	Sequence 2776, Ap
28	28	28.6	9	15	US-10-107-532-3286	Sequence 3286, Ap
29	28	28.6	9	15	US-10-107-532-3991	Sequence 3991, Ap
30	28	28.6	10	15	US-10-107-532-284	Sequence 284, App
31	28	28.6	10	15	US-10-107-532-896	Sequence 896, App
32	28	28.6	10	15	US-10-107-532-1418	Sequence 1418, Ap
33	28	28.6	10	15	US-10-107-532-1923	Sequence 1923, Ap
34	28	28.6	10	15	US-10-107-532-2499	Sequence 2499, Ap
35	28	28.6	10	15	US-10-107-532-3566	Sequence 3566, Ap
36	28	28.6	10	15	US-10-107-532-4968	Sequence 4968, Ap
37	28	28.6	10	15	US-10-107-532-5105	Sequence 5105, Ap
38	28	28.6	11	10	US-09-906-393A-9	Sequence 9, Appli
39	28	28.6	12	12	US-10-609-217-673	Sequence 673, App
40	28	28.6	12	12	US-10-609-217-683	Sequence 683, App
41	28	28.6	12	12	US-10-609-217-958	Sequence 958, App
42	28	28.6	12	12	US-10-632-388-673	Sequence 673, App
43	28	28.6	12	12	US-10-632-388-683	Sequence 683, App
44	28	28.6	12	12	US-10-632-388-958	Sequence 958, App
45	28	28.6	12	12	US-10-651-723-673	Sequence 673, App
46	28	28.6	12	12	US-10-651-723-683	Sequence 683, App
47	28	28.6	12	12	US-10-651-723-958	Sequence 958, App
48	28	28.6	12	12	US-10-645-761-673	Sequence 673, App
49	28	28.6	12	12	US-10-645-761-683	Sequence 683, App
50	28	28.6	12	12	US-10-645-761-958	Sequence 958, App
51	28	28.6	12	16	US-10-666-696-673	Sequence 673, App
52	28	28.6	12	16	US-10-666-696-683	Sequence 683, App
53	28	28.6	12	16	US-10-666-696-958	Sequence 958, App
54	28	28.6	12	16	US-10-653-048-673	Sequence 673, App
55	28	28.6	12	16	US-10-653-048-683	Sequence 683, App
56	28	28.6	12	16	US-10-653-048-958	Sequence 958, App

57	28	28.6	14	12	US-10-634-914-16	Sequence 16, Appl
58	28	28.6	15	15	US-10-107-532-5876	Sequence 5876, Ap
59	28	28.6	15	16	US-10-647-005-53	Sequence 53, Appl
60	28	28.6	16	12	US-10-609-217-786	Sequence 786, App
61	28	28.6	16	12	US-10-632-388-786	Sequence 786, App
62	28	28.6	16	12	US-10-651-723-786	Sequence 786, App
63	28	28.6	16	12	US-10-645-761-786	Sequence 786, App
64	28	28.6	16	16	US-10-666-696-786	Sequence 786, App
65	28	28.6	16	16	US-10-653-048-786	Sequence 786, App
66	28	28.6	17	12	US-10-609-217-785	Sequence 785, App
67	28	28.6	17	12	US-10-609-217-844	Sequence 844, App
68	28	28.6	17	12	US-10-609-217-847	Sequence 847, App
69	28	28.6	17	12	US-10-609-217-848	Sequence 848, App
70	28	28.6	17	12	US-10-632-388-785	Sequence 785, App
71	28	28.6	17	12	US-10-632-388-844	Sequence 844, App
72	28	28.6	17	12	US-10-632-388-847	Sequence 847, App
73	28	28.6	17	12	US-10-632-388-848	Sequence 848, App
74	28	28.6	17	12	US-10-651-723-785	Sequence 785, App
75	28	28.6	17	12	US-10-651-723-844	Sequence 844, App
76	28	28.6	17	12	US-10-651-723-847	Sequence 847, App
77	28	28.6	17	12	US-10-651-723-848	Sequence 848, App
78	28	28.6	17	12	US-10-645-761-785	Sequence 785, App
79	28	28.6	17	12	US-10-645-761-844	Sequence 844, App
80	28	28.6	17	12	US-10-645-761-847	Sequence 847, App
81	28	28.6	17	12	US-10-645-761-848	Sequence 848, App
82	28	28.6	17	14	US-10-161-791-338	Sequence 338, App
83	28	28.6	17	16	US-10-666-696-785	Sequence 785, App
84	28	28.6	17	16	US-10-666-696-844	Sequence 844, App
85	28	28.6	17	16	US-10-666-696-847	Sequence 847, App
86	28	28.6	17	16	US-10-666-696-848	Sequence 848, App
87	28	28.6	17	16	US-10-653-048-785	Sequence 785, App
88	28	28.6	17	16	US-10-653-048-844	Sequence 844, App
89	28	28.6	17	16	US-10-653-048-847	Sequence 847, App
90	28	28.6	17	16	US-10-653-048-848	Sequence 848, App
91	27	27.6	9	8	US-08-344-824-162	Sequence 162, App
92	27	27.6	9	12	US-09-891-823-122	Sequence 122, App
93	27	27.6	9	14	US-10-365-908-122	Sequence 122, App
94	27	27.6	9	14	US-10-357-175-148	Sequence 148, App
95	27	27.6	9	15	US-10-455-720-148	Sequence 148, App
96	27	27.6	9	15	US-10-149-138-4079	Sequence 4079, Ap
97	27	27.6	9	16	US-10-149-138-4079	Sequence 4079, Ap
98	27	27.6	10	8	US-08-344-824-251	Sequence 251, App
99	27	27.6	10	12	US-09-891-823-114	Sequence 114, App
100	27	27.6	10	12	US-10-601-100-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-10-281-652-3
; Sequence 3, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan

; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-10-281-652-3

  Query Match   100.0%; Score 98; DB 14; Length 18;
  Best Local Similarity   100.0%; Pred. No. 2.1e-07;
  Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 DQPPDVEKPDLQPFQVQS 18
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Db   1 DQPPDVEKPDLQPFQVQS 18

RESULT 2
US-10-014-340-759
; Sequence 759, Application US/10014340
; Publication No. US20030064411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor,
Including
; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 759
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-014-340-759

  Query Match   41.8%; Score 41; DB 12; Length 15;
  Best Local Similarity   47.1%; Pred. No. 27;
  Matches   8; Conservative   3; Mismatches   0; Indels   6; Gaps   1;

Qy   1 DQPPDVEKPDLQPFQVQ 17
              |||||:| ||::
Db   5 DQPPDIE------FQIR 15

RESULT 3
US-10-225-567A-1755
; Sequence 1755, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1755
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1755

Query Match 39.8%; Score 39; DB 14; Length 16;
Best Local Similarity 50.0%; Pred. No. 55;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Qy          2 QPPDVEKPDLQP 13
              :|||: | |  |
Db          5 RPPDIRKSDSSP 16
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RESULT 4
US-10-014-340-526
; Sequence 526, Application US/10014340
; Publication No. US20030064411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 526
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-526

Query Match 35.7%; Score 35; DB 12; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy          3 PPDVEKPDLQ 12
              ||  | |||:
Db          3 PPSAEYPDLR 12


RESULT 5
US-10-350-258-6
; Sequence 6, Application US/10350258
; Publication No. US20030139345A1
; GENERAL INFORMATION:
;  APPLICANT: MATTHIAS RATH
;  TITLE OF INVENTION: SYNTHETIC PEPTIDES AND METHODS FOR TREATING CANCER
INVASION AND METASTASIS
;  FILE REFERENCE: 11957/23
;  CURRENT APPLICATION NUMBER: US/10/350,258
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: 60/351,317
;  PRIOR FILING DATE: January 23, 2002
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-350-258-6

  Query Match             32.7%;  Score 32;  DB 14;  Length 9;
  Best Local Similarity   62.5%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 PPDVEKPD 10
              ||||:: |
Db          2 PPDVQRVD 9


RESULT 6
US-10-161-791-305
; Sequence 305, Application US/10161791
; Publication No. US20030186863A1
;  GENERAL INFORMATION:
;    APPLICANT:  SPARKS, Andrew B.
;    APPLICANT:  KAY, Brian K.
;    APPLICANT:  THORN, Judith M.
;    APPLICANT:  QUILLIAM, Lawrence A.
;    APPLICANT:  DER, Channing J.
;    APPLICANT:  FOWLKES, Dana M.
;    APPLICANT:  RIDER, James E.
;    TITLE OF INVENTION:  SH3 BINDING PEPTIDES AND METHODS OF
;    TITLE OF INVENTION:  ISOLATING AND USING SAME
;    NUMBER OF SEQUENCES:  467
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
```

; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 305:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-305

Query Match 32.7%; Score 32; DB 14; Length 18;
Best Local Similarity 43.8%; Pred. No. 6.4e+02;
Matches 7; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy          2 QPPDVEKPDLQPFQVQ 17
              |||    |  ||   |
Db          3 QPPYFPPPPYQPIYPQ 18
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RESULT 7
US-09-572-404B-3283
; Sequence 3283, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3283
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in DAF OR CD55 at 291-300 and may interact with

; OTHER INFORMATION: Sequence 3284 in this patent.
US-09-572-404B-3283

  Query Match   31.6%; Score 31; DB 10; Length 10;
  Best Local Similarity   71.4%; Pred. No. 4.7e+02;
  Matches   5; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   3 PPDVEKP 9
              || |:||
Db   3 PPTVQKP 9

RESULT 8
US-10-601-837-34
; Sequence 34, Application US/10601837
; Publication No. US20040053309A1
; GENERAL INFORMATION:
; APPLICANT: Holt, Gordon D
; APPLICANT: Kelly, Michael D
; APPLICANT: Kennedy, Sandra J
; APPLICANT: Moyses, Christopher
; TITLE OF INVENTION: Proteins, Genes and Their Use for Diagnosis and Treatment
of Kidney
; TITLE OF INVENTION: Response
; FILE REFERENCE: 2543-1-030
; CURRENT APPLICATION NUMBER: US/10/601,837
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: PCT/GB01/05777
; PRIOR FILING DATE: 2001-12-24
; PRIOR APPLICATION NUMBER: US 60/260392
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Ratus No. US20040053309A1vegicus
US-10-601-837-34

  Query Match   31.6%; Score 31; DB 12; Length 11;
  Best Local Similarity   55.6%; Pred. No. 5.2e+02;
  Matches   5; Conservative   2; Mismatches   2; Indels   0; Gaps   0;

Qy   7 EKPDLQPFQ 15
              : |:| |||
Db   2 DNPNLPPFQ 10

RESULT 9
US-10-022-066-144
; Sequence 144, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLIMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; TITLE OF INVENTION: USES THEREOF

; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022,066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 144
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: peptide
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: Unknown amino acid
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (3)
;   OTHER INFORMATION: Unknown amino acid
US-10-022-066-144

  Query Match   30.6%; Score 30; DB 14; Length 11;
  Best Local Similarity   57.1%; Pred. No. 7.3e+02;
  Matches   4; Conservative   2; Mismatches   1; Indels   0; Gaps   0;

Qy   1 DQPPDVE 7
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Db   4 DPPPDMZ 10

RESULT 10
US-10-022-066-374
; Sequence 374, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLIMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022,066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17

; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 374
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: peptide
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: Unknown amino acid
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (3)
;   OTHER INFORMATION: Unknown amino acid
US-10-022-066-374

  Query Match   30.6%; Score 30; DB 14; Length 11;
  Best Local Similarity   57.1%; Pred. No. 7.3e+02;
  Matches   4; Conservative   2; Mismatches   1; Indels   0; Gaps   0;

Qy   1 DQPPDVE 7
              | |||::
Db   4 DPPPDMZ 10

RESULT 11
US-10-149-138-3845
; Sequence 3845, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3845
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3845

  Query Match   30.6%; Score 30; DB 15; Length 15;
  Best Local Similarity   45.5%; Pred. No. 1e+03;
  Matches   5; Conservative   3; Mismatches   3; Indels   0; Gaps   0;

Qy   3 PPDVEKPDLQP 13
              | | :||::|
Db   1 PEYVNQPDVRP 11

RESULT 12
US-10-149-138-3845
; Sequence 3845, Application US/10149138
; Publication No. US20040121946A9
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3845
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3845

  Query Match   30.6%; Score 30; DB 16; Length 15;
  Best Local Similarity   45.5%; Pred. No. 1e+03;
  Matches   5; Conservative   3; Mismatches   3; Indels   0; Gaps   0;

Qy   3 PPDVEKPDLQP 13
              | | :||::|
Db   1 PEYVNQPDVRP 11

RESULT 13
US-09-891-823-98
; Sequence 98, Application US/09891823
; Publication No. US20020110566A1

; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/09/891,823
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-09-891-823-98

Query Match 29.6%; Score 29; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPDV 6
||||||
Db 2 QPPDV 6

RESULT 14
US-10-365-908-98
; Sequence 98, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-98

Query Match 29.6%; Score 29; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 QPPDV 6
              |||||
Db          2 QPPDV 6
```

RESULT 15
US-10-033-662-36
; Sequence 36, Application US/10033662
; Publication No. US20030092197A1
; GENERAL INFORMATION:
; APPLICANT: Herman, et al.
; TITLE OF INVENTION: Proteins, Genes and Their Use For Diagnosis and Treatment of Cardiac
; TITLE OF INVENTION: Response
; FILE REFERENCE: 9195-081
; CURRENT APPLICATION NUMBER: US/10/033,662
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-033-662-36

Query Match 29.6%; Score 29; DB 14; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          8 KPDLQP 13
              |||| |
Db          1 KPDLSP 6
```

RESULT 16
US-09-572-404B-3027
; Sequence 3027, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3027
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in GUCY2D OR GUC2D OR RETGC1 OR RETGC OR GUC1A4 OR
; OTHER INFORMATION: CORD6 at 1069-1078 and may interact with Sequence 3028 in this patent.

US-09-572-404B-3027

  Query Match 29.6%; Score 29; DB 10; Length 10;
  Best Local Similarity 100.0%; Pred. No. 9.2e+02;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          9 PDLQP 13
              |||||
Db          2 PDLQP 6
```

RESULT 17
US-09-992-665-47
; Sequence 47, Application US/09992665
; Publication No. US20030092009A1
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: CEMINES.002A
; CURRENT APPLICATION NUMBER: US/09/992,665
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Probe
US-09-992-665-47

  Query Match 29.6%; Score 29; DB 10; Length 13;
  Best Local Similarity 41.7%; Pred. No. 1.2e+03;
  Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

```
Qy          2 QPPDVEKPDLQP 13
              ||| :  |   |
Db          1 QPPSMSSPPPPP 12
```

RESULT 18
US-10-080-608A-70
; Sequence 70, Application US/10080608A
; Publication No. US20030198956A1
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/10/080,608A
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 70
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human rhinovirus 2
US-10-080-608A-70

  Query Match 29.6%; Score 29; DB 14; Length 15;
  Best Local Similarity 100.0%; Pred. No. 1.4e+03;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDLQP 13
      |||||
Db 9 PDLQP 13

RESULT 19
US-10-370-685-159
; Sequence 159, Application US/10370685
; Publication No. US20030215903A1
; GENERAL INFORMATION:
; APPLICANT: Hyman, Paul
; APPLICANT: Goldberg, Edward
; TITLE OF INVENTION: Nanostructures Containing PNA Joining and Functional
Elements
; FILE REFERENCE: NANF.P-004
; CURRENT APPLICATION NUMBER: US/10/370,685
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,608
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 159
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human rhinovirus 2
US-10-370-685-159

  Query Match 29.6%; Score 29; DB 15; Length 15;
  Best Local Similarity 100.0%; Pred. No. 1.4e+03;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDLQP 13
      |||||
Db 9 PDLQP 13

RESULT 20
US-10-371-067-1
; Sequence 1, Application US/10371067
; Publication No. US20040018587A1
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Williams, Mark K
; APPLICANT: Goldberg, Edward B
; TITLE OF INVENTION: Nanostructures containing antibody assembly subunits
; FILE REFERENCE: NANF.P-003
; CURRENT APPLICATION NUMBER: US/10/371,067

; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,608
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/136,225
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 09/236,949
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/542,003
; PRIOR FILING DATE: 1995-10-12
; PRIOR APPLICATION NUMBER: 08/322,760
; PRIOR FILING DATE: 1994-10-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: (Antibody 8F5) Complexed With Peptide From Human
Rhinovirus
;   OTHER INFORMATION: (Serotype 2) Viral Capsid Protein Vp2 (Residues 156 -170)
US-10-371-067-1

  Query Match   29.6%; Score 29; DB 15; Length 15;
  Best Local Similarity   100.0%; Pred. No. 1.4e+03;
  Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   9 PDLQP 13
              |||||
Db   9 PDLQP 13

RESULT 21
US-10-225-567A-1370
; Sequence 1370, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED
RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1370
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-225-567A-1370

  Query Match   29.6%; Score 29; DB 14; Length 17;

Best Local Similarity 41.7%; Pred. No. 1.6e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
Qy          7 EKPDLQPFQVQS 18
              : ||||  :: |
Db          6 KNPDLQAIRIAS 17
```

RESULT 22
US-10-443-349-12
; Sequence 12, Application US/10443349
; Publication No. US20040023856A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert E.
; APPLICANT: Wagman, David W.
; TITLE OF INVENTION: B1k CHAIN OF LAMININ AND METHODS OF USE
; FILE REFERENCE: 10287/021003
; CURRENT APPLICATION NUMBER: US/10/443,349
; CURRENT FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: US/09/161,872
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 08/735,893
; PRIOR FILING DATE: 1996-10-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-443-349-12

Query Match 29.6%; Score 29; DB 16; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 DQPPDVEKPD 10
              |: ||:|  |
Db          1 DENPDIECAD 10
```

RESULT 23
US-09-922-261-200
; Sequence 200, Application US/09922261
; Patent No. US20020111471A1
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES
INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999

; CURRENT APPLICATION NUMBER: US/09/922,261
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US/09/461,697
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 200
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-922-261-200

  Query Match   29.6%; Score 29; DB 9; Length 18;
  Best Local Similarity   54.5%; Pred. No. 1.7e+03;
  Matches   6; Conservative   2; Mismatches   3; Indels   0; Gaps   0;

Qy   6 VEKPDLQPFQV 16
              :||| || |:
Db   1 MEKPKLQRHQL 11

RESULT 24
US-10-107-532-25
; Sequence 25, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of
Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-107-532-25

  Query Match   28.6%; Score 28; DB 15; Length 9;
  Best Local Similarity   62.5%; Pred. No. 1.2e+06;
  Matches   5; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

```
Qy          2 QPPDVEKP 9
              ||  :|||
Db          1 QPEPLEKP 8


RESULT 25
US-10-107-532-652
; Sequence 652, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
;  APPLICANT: Agensys, Inc.
;  APPLICANT:  Jakobovits, Aya
;  APPLICANT:  Faris, Mary
;  APPLICANT:  Morrison, Karen Jane Meyrick
;  APPLICANT:  Morrison, Robert Kendall
;  APPLICANT:  Hubert, Rene S.
;  APPLICANT:  Afar, Daniel E.H.
;  APPLICANT:  Ge, Wangmao
;  APPLICANT:  Raitano, Arthur
;  APPLICANT:  Challita-Eid, Pia M.
;  TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
;  TITLE OF INVENTION:  Entitled 158P3D2 Useful in Treatment and Detection of
Cancer
;  FILE REFERENCE: 51158-200064.00
;  CURRENT APPLICATION NUMBER: US/10/107,532
;  CURRENT FILING DATE:  2002-08-05
;  PRIOR APPLICATION NUMBER: 60/283,112
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/286,630
;  PRIOR FILING DATE: 2001-04-25
;  NUMBER OF SEQ ID NOS: 6321
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 652
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-107-532-652

  Query Match             28.6%;  Score 28;  DB 15;  Length 9;
  Best Local Similarity   62.5%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 QPPDVEKP 9
              ||  :|||
Db          2 QPEPLEKP 9


RESULT 26
US-10-107-532-2214
; Sequence 2214, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
;  APPLICANT: Agensys, Inc.
;  APPLICANT:  Jakobovits, Aya
;  APPLICANT:  Faris, Mary
;  APPLICANT:  Morrison, Karen Jane Meyrick
```

; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2214
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-2214

Query Match 28.6%; Score 28; DB 15; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 QPPDVEKP 9
              ||  :|||
Db          1 QPEPLEKP 8
```

RESULT 27
US-10-107-532-2776
; Sequence 2776, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630

; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2776
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-107-532-2776

  Query Match   28.6%; Score 28; DB 15; Length 9;
  Best Local Similarity   62.5%; Pred. No. 1.2e+06;
  Matches   5; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

Qy   2 QPPDVEKP 9
              || :|||
Db   1 QPEPLEKP 8

RESULT 28
US-10-107-532-3286
; Sequence 3286, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of
Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3286
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-107-532-3286

  Query Match   28.6%; Score 28; DB 15; Length 9;
  Best Local Similarity   62.5%; Pred. No. 1.2e+06;
  Matches   5; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

Qy   2 QPPDVEKP 9
              || :|||

```
Db          1 QPEPLEKP 8


RESULT 29
US-10-107-532-3991
; Sequence 3991, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
;  APPLICANT: Agensys, Inc.
;  APPLICANT:  Jakobovits, Aya
;  APPLICANT:  Faris, Mary
;  APPLICANT:  Morrison, Karen Jane Meyrick
;  APPLICANT:  Morrison, Robert Kendall
;  APPLICANT:  Hubert, Rene S.
;  APPLICANT:  Afar, Daniel E.H.
;  APPLICANT:  Ge, Wangmao
;  APPLICANT:  Raitano, Arthur
;  APPLICANT:  Challita-Eid, Pia M.
;  TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
;  TITLE OF INVENTION:  Entitled 158P3D2 Useful in Treatment and Detection of
Cancer
;  FILE REFERENCE: 51158-200064.00
;  CURRENT APPLICATION NUMBER: US/10/107,532
;  CURRENT FILING DATE:  2002-08-05
;  PRIOR APPLICATION NUMBER: 60/283,112
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/286,630
;  PRIOR FILING DATE: 2001-04-25
;  NUMBER OF SEQ ID NOS: 6321
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3991
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-107-532-3991

  Query Match             28.6%;  Score 28;  DB 15;  Length 9;
  Best Local Similarity   62.5%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 QPPDVEKP 9
              ||  :|||
Db          1 QPEPLEKP 8


RESULT 30
US-10-107-532-284
; Sequence 284, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
;  APPLICANT: Agensys, Inc.
;  APPLICANT:  Jakobovits, Aya
;  APPLICANT:  Faris, Mary
;  APPLICANT:  Morrison, Karen Jane Meyrick
;  APPLICANT:  Morrison, Robert Kendall
;  APPLICANT:  Hubert, Rene S.
;  APPLICANT:  Afar, Daniel E.H.
```

; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 284
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-284

Query Match 28.6%; Score 28; DB 15; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9
|| :|||
Db 1 QPEPLEKP 8

RESULT 31
US-10-107-532-896
; Sequence 896, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 896
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-896

  Query Match 28.6%; Score 28; DB 15; Length 10;
  Best Local Similarity 62.5%; Pred. No. 1.3e+03;
  Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9
      || :|||
Db 2 QPEPLEKP 9

RESULT 32
US-10-107-532-1418
; Sequence 1418, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of
Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1418
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-1418

  Query Match 28.6%; Score 28; DB 15; Length 10;
  Best Local Similarity 62.5%; Pred. No. 1.3e+03;
  Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9
      || :|||
Db 1 QPEPLEKP 8

RESULT 33
US-10-107-532-1923
; Sequence 1923, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of
Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1923
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-107-532-1923

  Query Match   28.6%; Score 28; DB 15; Length 10;
  Best Local Similarity   62.5%; Pred. No. 1.3e+03;
  Matches   5; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

Qy   2 QPPDVEKP 9
              || :|||
Db   1 QPEPLEKP 8

RESULT 34
US-10-107-532-2499
; Sequence 2499, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.

; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2499
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-2499

Query Match 28.6%; Score 28; DB 15; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 QPPDVEKP 9
              ||  :|||
Db          2 QPEPLEKP 9
```

RESULT 35
US-10-107-532-3566
; Sequence 3566, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3566
; LENGTH: 10
; TYPE: PRT

; ORGANISM: Homo sapien
US-10-107-532-3566

  Query Match 28.6%; Score 28; DB 15; Length 10;
  Best Local Similarity 62.5%; Pred. No. 1.3e+03;
  Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9
      || :|||
Db 2 QPEPLEKP 9

RESULT 36
US-10-107-532-4968
; Sequence 4968, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of
Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4968
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-107-532-4968

  Query Match 28.6%; Score 28; DB 15; Length 10;
  Best Local Similarity 62.5%; Pred. No. 1.3e+03;
  Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9
      || :|||
Db 1 QPEPLEKP 8

RESULT 37
US-10-107-532-5105
; Sequence 5105, Application US/10107532

; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5105
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-5105

Query Match 28.6%; Score 28; DB 15; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 QPPDVEKP 9
              ||  :|||
Db          1 QPEPLEKP 8
```

RESULT 38
US-09-906-393A-9
; Sequence 9, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-906-393A-9

  Query Match   28.6%; Score 28; DB 10; Length 11;
  Best Local Similarity   57.1%; Pred. No. 1.4e+03;
  Matches   4; Conservative   2; Mismatches   1; Indels   0; Gaps   0;

Qy   4 PDVEKPD 10
              || :||:
Db   1 PDAKKPE 7

RESULT 39
US-10-609-217-673
; Sequence 673, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 673
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-609-217-673

  Query Match   28.6%; Score 28; DB 12; Length 12;
  Best Local Similarity   71.4%; Pred. No. 1.6e+03;
  Matches   5; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   12 QPFQVQS 18
              ||: |||
Db   6 QPYSVQS 12

RESULT 40
US-10-609-217-683
; Sequence 683, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES

```
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/609,217
;  CURRENT FILING DATE:  2003-06-27
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 683
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-609-217-683

  Query Match             28.6%;  Score 28;  DB 12;  Length 12;
  Best Local Similarity   71.4%;  Pred. No. 1.6e+03;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 QPFQVQS 18
                ||: |||
Db          6 QPYSVQS 12


RESULT 41
US-10-609-217-958
; Sequence 958, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/609,217
;  CURRENT FILING DATE:  2003-06-27
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 958
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5)..(5)
;   OTHER INFORMATION: Position 5, Xaa = naphthylalanine
US-10-609-217-958
```

```
  Query Match             28.6%;  Score 28;  DB 12;  Length 12;
  Best Local Similarity   71.4%;  Pred. No. 1.6e+03;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 QPFQVQS 18
              ||: |||
Db          6 QPYSVQS 12


RESULT 42
US-10-632-388-673
; Sequence 673, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/632,388
;  CURRENT FILING DATE:  2003-07-31
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 673
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-632-388-673

  Query Match             28.6%;  Score 28;  DB 12;  Length 12;
  Best Local Similarity   71.4%;  Pred. No. 1.6e+03;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 QPFQVQS 18
              ||: |||
Db          6 QPYSVQS 12


RESULT 43
US-10-632-388-683
; Sequence 683, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
```

; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 683
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-632-388-683

  Query Match   28.6%; Score 28; DB 12; Length 12;
  Best Local Similarity   71.4%; Pred. No. 1.6e+03;
  Matches   5; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   12 QPFQVQS 18
              ||: |||
Db   6 QPYSVQS 12

RESULT 44
US-10-632-388-958
; Sequence 958, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 958
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5)..(5)
;   OTHER INFORMATION: Position 5, Xaa = naphthylalanine
US-10-632-388-958

  Query Match   28.6%; Score 28; DB 12; Length 12;

Best Local Similarity 71.4%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          12 QPFQVQS 18
               ||: |||
Db           6 QPYSVQS 12
```

RESULT 45
US-10-651-723-673
; Sequence 673, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 673
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-651-723-673

Query Match 28.6%; Score 28; DB 12; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          12 QPFQVQS 18
               ||: |||
Db           6 QPYSVQS 12
```

RESULT 46
US-10-651-723-683
; Sequence 683, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29

; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 683
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-651-723-683

  Query Match   28.6%; Score 28; DB 12; Length 12;
  Best Local Similarity   71.4%; Pred. No. 1.6e+03;
  Matches   5; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   12 QPFQVQS 18
              ||: |||
Db   6 QPYSVQS 12

RESULT 47
US-10-651-723-958
; Sequence 958, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 958
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5)..(5)
;   OTHER INFORMATION: Position 5, Xaa = naphthylalanine
US-10-651-723-958

  Query Match   28.6%; Score 28; DB 12; Length 12;
  Best Local Similarity   71.4%; Pred. No. 1.6e+03;
  Matches   5; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

```
Qy          12 QPFQVQS 18
               ||: |||
Db           6 QPYSVQS 12


RESULT 48
US-10-645-761-673
; Sequence 673, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/645,761
;  CURRENT FILING DATE:  2003-08-18
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 673
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-645-761-673

  Query Match             28.6%;  Score 28;  DB 12;  Length 12;
  Best Local Similarity   71.4%;  Pred. No. 1.6e+03;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 QPFQVQS 18
               ||: |||
Db           6 QPYSVQS 12


RESULT 49
US-10-645-761-683
; Sequence 683, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/645,761
;  CURRENT FILING DATE:  2003-08-18
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
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; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 683
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-645-761-683

  Query Match   28.6%; Score 28; DB 12; Length 12;
  Best Local Similarity   71.4%; Pred. No. 1.6e+03;
  Matches   5; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   12 QPFQVQS 18
              ||: |||
Db   6 QPYSVQS 12

RESULT 50
US-10-645-761-958
; Sequence 958, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 958
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5)..(5)
;   OTHER INFORMATION: Position 5, Xaa = naphthylalanine
US-10-645-761-958

  Query Match   28.6%; Score 28; DB 12; Length 12;
  Best Local Similarity   71.4%; Pred. No. 1.6e+03;
  Matches   5; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   12 QPFQVQS 18

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                ||: |||
Db            6 QPYSVQS 12


Search completed: July  4, 2004, 05:12:24
Job time : 36.3284 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:33:51 ; Search time 30.6269 Seconds
(without alignments)
185.436 Million cell updates/sec

Title: US-09-641-802-3
Perfect score: 98
Sequence: 1 DQPPDVEKPDLQPFQVQS 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 5664

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description

1	31	31.6	18	6	P82674	P82674 bos taurus
2	29	29.6	15	8	Q9T2K8	Q9t2k8 spinacia ol
3	29	29.6	17	15	Q8UT86	Q8ut86 human immun
4	28.5	29.1	17	4	Q9UDD6	Q9udd6 homo sapien
5	28	28.6	18	2	Q9R4E0	Q9r4e0 pseudomonas
6	28	28.6	18	13	O13167	O13167 xiphias gla
7	27	27.6	10	13	Q9PRY8	Q9pry8 triakis scy
8	27	27.6	12	10	P82325	P82325 pisum sativ
9	27	27.6	16	4	Q9UCI2	Q9uci2 homo sapien
10	27	27.6	18	5	Q8MNX0	Q8mnx0 bombyx mori
11	27	27.6	18	10	Q9S8G8	Q9s8g8 psophocarpu
12	26	26.5	13	4	Q9UEE2	Q9uee2 homo sapien
13	26	26.5	15	1	Q9UWH3	Q9uwh3 thermococcu
14	26	26.5	15	6	Q9TR14	Q9tr14 bos taurus
15	26	26.5	17	11	Q9JK08	Q9jk08 mus musculu
16	26	26.5	17	15	P90402	P90402 human immun
17	26	26.5	17	15	Q9Q709	Q9q709 human immun
18	26	26.5	18	2	Q9X3E9	Q9x3e9 prochloroco
19	26	26.5	18	5	Q9TWL5	Q9twl5 lucilia cup
20	25.5	26.0	17	10	P83061	P83061 spinacia ol
21	25	25.5	18	4	Q9UCT9	Q9uct9 homo sapien
22	24	24.5	11	2	Q9S618	Q9s618 prochloroco
23	24	24.5	12	10	P82328	P82328 pisum sativ
24	24	24.5	13	2	Q9R3R6	Q9r3r6 prochloroco
25	24	24.5	17	2	Q9LB06	Q9lb06 prochloroco
26	24	24.5	18	2	O67971	O67971 synechococc
27	23.5	24.0	9	4	Q9UCS8	Q9ucs8 homo sapien
28	23	23.5	9	2	Q9R735	Q9r735 streptomyce
29	23	23.5	14	2	P81715	P81715 streptomyce
30	23	23.5	17	2	P97135	P97135 mycobacteri
31	23	23.5	18	8	Q7YMC5	Q7ymc5 pogonatum s
32	22	22.4	10	2	Q9L5W6	Q9l5w6 liberibacte
33	22	22.4	11	6	Q8HYM4	Q8hym4 felis silve
34	22	22.4	14	11	Q9R1U3	Q9r1u3 rattus norv
35	22	22.4	15	2	O69142	O69142 streptococc
36	22	22.4	15	10	Q08936	Q08936 nicotiana t
37	22	22.4	16	11	Q9QVL2	Q9qvl2 mus sp. mep
38	22	22.4	17	2	Q9EUP4	Q9eup4 thermus the
39	22	22.4	17	6	O46667	O46667 macropus ro
40	22	22.4	17	6	Q95M99	Q95m99 equus cabal
41	22	22.4	17	11	Q9QVC6	Q9qvc6 rattus norv
42	22	22.4	17	11	Q9QVC2	Q9qvc2 rattus sp.
43	22	22.4	17	12	Q919B0	Q919b0 human papil
44	22	22.4	18	2	Q56610	Q56610 vibrio chol
45	22	22.4	18	4	Q9P0M3	Q9p0m3 homo sapien
46	22	22.4	18	4	Q96C65	Q96c65 homo sapien
47	22	22.4	18	11	Q9WTP8	Q9wtp8 rattus norv
48	22	22.4	18	12	Q919D5	Q919d5 human papil
49	22	22.4	18	12	Q919B3	Q919b3 human papil
50	22	22.4	18	12	Q919B5	Q919b5 human papil
51	22	22.4	18	12	Q919B7	Q919b7 human papil
52	22	22.4	18	12	Q919C5	Q919c5 human papil
53	22	22.4	18	12	Q919D1	Q919d1 human papil
54	22	22.4	18	12	Q919D3	Q919d3 human papil
55	22	22.4	18	12	Q919B9	Q919b9 human papil
56	22	22.4	18	12	Q919A8	Q919a8 human papil
57	22	22.4	18	12	Q919C7	Q919c7 human papil

58	22	22.4	18	12	Q919C9	Q919c9 human papil
59	21.5	21.9	17	6	Q95KQ7	Q95kq7 sus scrofa
60	21	21.4	9	10	P82429	P82429 nicotiana t
61	21	21.4	10	8	Q8SHA8	Q8sha8 rhampholeon
62	21	21.4	13	6	Q9TQS4	Q9tqs4 equus cabal
63	21	21.4	13	6	Q865C9	Q865c9 sus scrofa
64	21	21.4	13	8	Q9T2U1	Q9t2u1 bos taurus
65	21	21.4	14	5	Q26075	Q26075 psammechinu
66	21	21.4	14	11	Q9JJU5	Q9jju5 mus musculu
67	21	21.4	16	2	Q9R596	Q9r596 micrococcus
68	21	21.4	16	8	Q8HU27	Q8hu27 passiflora
69	21	21.4	16	8	Q8HU26	Q8hu26 passiflora
70	21	21.4	16	11	Q9QUW5	Q9quw5 rattus sp.
71	21	21.4	16	11	Q9QUW8	Q9quw8 cavia (guin
72	21	21.4	17	2	Q8VME2	Q8vme2 pseudomonas
73	21	21.4	17	6	Q9TRW1	Q9trw1 oryctolagus
74	21	21.4	18	6	Q9TT81	Q9tt81 bos taurus
75	21	21.4	18	11	Q9QZX4	Q9qzx4 mus spretus
76	21	21.4	18	11	Q9QZX5	Q9qzx5 mus musculu
77	20	20.4	8	11	Q80XV8	Q80xv8 rattus sp.
78	20	20.4	9	4	Q16605	Q16605 homo sapien
79	20	20.4	10	11	Q63056	Q63056 rattus norv
80	20	20.4	13	11	Q9QVL4	Q9qvl4 rattus sp.
81	20	20.4	13	11	O88176	O88176 mus musculu
82	20	20.4	15	2	Q9KIV5	Q9kiv5 anabaena sp
83	20	20.4	15	5	Q9TWT4	Q9twt4 lumbricus t
84	20	20.4	15	10	Q9AT15	Q9at15 lycopersico
85	20	20.4	15	10	P82431	P82431 nicotiana t
86	20	20.4	15	11	Q62531	Q62531 mus spretus
87	20	20.4	15	11	Q8CJ29	Q8cj29 mus musculu
88	20	20.4	16	5	Q9TWN7	Q9twn7 toxoplasma
89	20	20.4	16	6	Q9TR97	Q9tr97 oryctolagus
90	20	20.4	17	4	Q16231	Q16231 homo sapien
91	20	20.4	17	4	Q9UEJ5	Q9uej5 homo sapien
92	20	20.4	17	5	Q9TWB9	Q9twb9 acanthamoeb
93	20	20.4	17	8	Q85UP3	Q85up3 acrocladium
94	20	20.4	17	8	Q7YMZ4	Q7ymz4 porothamniu
95	20	20.4	17	8	Q7YMZ1	Q7ymz1 porotrichum
96	20	20.4	17	11	Q9QVK3	Q9qvk3 rattus sp.
97	20	20.4	18	2	Q8VNJ9	Q8vnj9 haemophilus
98	20	20.4	18	2	Q9R5B0	Q9r5b0 arthrobacte
99	20	20.4	18	4	Q8NFB4	Q8nfb4 homo sapien
100	20	20.4	18	6	Q9TQR9	Q9tqr9 mammuthus p

ALIGNMENTS

RESULT 1
P82674
ID   P82674   PRELIMINARY;   PRT;   18 AA.
AC   P82674;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Mitochondrial 28S ribosomal protein S5 (MRP-S5) (Fragments).
OS   Bos taurus (Bovine).

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Liver;
RA   Koc E.C., Burkhart W., Blackburn K., Moseley A., Koc H.,
RA   Spremulli L.L.;
RT   "Identification of four proteins from the small subunit of the
RT   mammalian mitochondrial ribosome using a proteomics approach.";
RL   Submitted (JUL-2000) to Swiss-Prot.
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
CC   -!- MASS SPECTROMETRY: MW=974.58; METHOD=ELECTROSPRAY; RANGE=1-8.
CC   -!- SIMILARITY: BELONGS TO THE S5P FAMILY OF RIBOSOMAL PROTEINS.
DR   GO; GO:0005739; C:mitochondrion; IEA.
DR   GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR   InterPro; IPR000851; Ribosomal_S5.
DR   PROSITE; PS00585; RIBOSOMAL_S5; PARTIAL.
KW   Ribosomal protein; Mitochondrion.
FT   NON_TER       1      1
FT   NON_CONS      8      9
FT   UNSURE       17     17       OR I.
FT   NON_TER      18     18
SQ   SEQUENCE   18 AA;  2127 MW;  199BC913E7E25FAF CRC64;

  Query Match             31.6%;  Score 31;  DB 6;  Length 18;
  Best Local Similarity   66.7%;  Pred. No. 4.5e+02;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 PDVEKPDLQ 12
              |: | ||||
Db         10 PEDEVPDLQ 18


RESULT 2
Q9T2K8
ID   Q9T2K8      PRELIMINARY;      PRT;    15 AA.
AC   Q9T2K8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   LHCII kinase, 64 kDa kinase (Fragment).
OS   Spinacia oleracea (Spinach).
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Caryophyllales; Amaranthaceae; Spinacia.
OX   NCBI_TaxID=3562;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92183823; PubMed=1544419;
RA   Gal A., Herrmann R.G., Lottspeich F., Ohad I.;
RT   "Phosphorylation of cytochrome b6 by the LHC II kinase associated with
RT   the cytochrome complex.";
RL   FEBS Lett. 298:33-35(1992).
DR   PIR; S20410; S20410.
```

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DR   PIR; S66419; S66419.
FT   NON_TER       1      1
FT   NON_TER      15     15
SQ   SEQUENCE   15 AA;  1556 MW;  6E00A4F917DDF33E CRC64;

  Query Match             29.6%;  Score 29;  DB 8;  Length 15;
  Best Local Similarity   75.0%;  Pred. No. 7.7e+02;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 PDVEKPDL 11
              |||||  |
Db          5 PDVEKSTL 12


RESULT 3
Q8UT86
ID   Q8UT86      PRELIMINARY;      PRT;    17 AA.
AC   Q8UT86;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vpr protein.
GN   VPR.
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=00BW1795.6;
RA   Novitsky V.A., Smith U.R., Gilbert P., McLane M.F., Chigwedere P.,
RA   Williamson C., Ndung'u T., Klein I., Chang S.-Y., Peter T., Thior I.,
RA   Foley B.T., Gaolekwe S., Rybak N., Gaseitsiwe S., Vannberg F.,
RA   Marlink R., Lee T.-H., Essex M.;
RT   "HIV-1 subtype C molecular phylogeny: consensus sequence for an AIDS
RT   vaccine design.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF443097; AAL34763.1; -.
DR   InterPro; IPR000012; RetroV_VpR/X.
DR   Pfam; PF00522; VPR; 1.
KW   AIDS.
SQ   SEQUENCE   17 AA;  2018 MW;  58CA6A463F4457C7 CRC64;

  Query Match             29.6%;  Score 29;  DB 15;  Length 17;
  Best Local Similarity   28.6%;  Pred. No. 8.7e+02;
  Matches    4;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DQPPDVEKPDLQPF 14
              :| |: : |  :|:
Db          2 EQAPEDQGPQREPY 15


RESULT 4
Q9UDD6
ID   Q9UDD6      PRELIMINARY;      PRT;    17 AA.
AC   Q9UDD6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Fatty acid ETHYL ester synthase-II, FAEE synthase-II (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92317032; PubMed=1618826;
RA   Bora P.S., Wu X., Spilburg C.A., Lange L.G.;
RT   "Purification and characterization of fatty acid ethyl ester synthase-
RT   II from human myocardium.";
RL   J. Biol. Chem. 267:13217-13221(1992).
DR   PIR; A42920; A42920.
DR   GO; GO:0005829; C:cytosol; NAS.
DR   GO; GO:0030339; F:fatty-acyl-ethyl-ester synthase activity; NAS.
DR   GO; GO:0006067; P:ethanol metabolism; NAS.
DR   GO; GO:0006631; P:fatty acid metabolism; NAS.
FT   NON_TER       1      1
FT   NON_TER      17     17
SQ   SEQUENCE   17 AA;  1755 MW;  3456973BF1B39273 CRC64;

  Query Match             29.1%;  Score 28.5;  DB 4;  Length 17;
  Best Local Similarity   46.2%;  Pred. No. 1e+03;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    3;  Gaps    1;

Qy          1 DQPPDVEKPDLQP 13
              : |||   ||  |
Db          1 EDPPD---PDTTP 10


RESULT 5
Q9R4E0
ID   Q9R4E0      PRELIMINARY;      PRT;    18 AA.
AC   Q9R4E0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Dipeptidyl aminopeptidase type I (Fragment).
OS   Pseudomonas.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae.
OX   NCBI_TaxID=286;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=96200096; PubMed=8631703;
RA   Ogasawara W., Ochiai K., Ando K., Yano K., Yamasaki M., Okada H.,
RA   Morikawa Y.;
RT   "A novel dipeptidyl aminopeptidase from Pseudomonas sp. strain WO24.";
RL   J. Bacteriol. 178:1283-1288(1996).
SQ   SEQUENCE   18 AA;  1813 MW;  369B0388C394A737 CRC64;

  Query Match             28.6%;  Score 28;  DB 2;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.3e+03;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 PPDVEK 8
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              |||| |
Db          5 PPDVAK 10


RESULT 6
O13167
ID   O13167      PRELIMINARY;      PRT;    18 AA.
AC   O13167;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Ribosomal protein S7 (Fragment).
OS   Xiphias gladius (Swordfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC   Xiphiidae; Xiphias.
OX   NCBI_TaxID=8245;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VARIOUS STRAINS;
RA   Chow S.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=J26B;
RA   Chow S.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U95521; AAB58281.1; -.
DR   EMBL; U89244; AAB58379.1; -.
DR   EMBL; U95515; AAB58275.1; -.
DR   EMBL; U95516; AAB58276.1; -.
DR   EMBL; U95517; AAB58277.1; -.
DR   EMBL; U95518; AAB58278.1; -.
DR   EMBL; U95519; AAB58279.1; -.
DR   EMBL; U95520; AAB58280.1; -.
DR   GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW   Ribosomal protein.
FT   NON_TER      18      18
SQ   SEQUENCE   18 AA;  1978 MW;  E716F226CC5BEB15 CRC64;

  Query Match             28.6%;  Score 28;  DB 13;  Length 18;
  Best Local Similarity   71.4%;  Pred. No. 1.3e+03;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 PDVEKPD 10
              |: ||||
Db         11 PNGEKPD 17


RESULT 7
Q9PRY8
ID   Q9PRY8      PRELIMINARY;      PRT;    10 AA.
AC   Q9PRY8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
```

```
DE   Angiotensin I.
OS   Triakis scyllium (Leopard shark) (Triakis scyllia).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;
OC   Triakis.
OX   NCBI_TaxID=30494;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94141412; PubMed=8308464;
RA   Takei Y., Hasegawa Y., Watanabe T.X., Nakajima K., Hazon N.;
RT   "A novel angiotensin I isolated from an elasmobranch fish.";
RL   J. Endocrinol. 139:281-285(1993).
SQ   SEQUENCE   10 AA;  1284 MW;  20F02FD761E04B47 CRC64;

  Query Match             27.6%;  Score 27;  DB 13;  Length 10;
  Best Local Similarity   44.4%;  Pred. No. 1e+03;
  Matches    4;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 KPDLQPFQV 16
              :| : |||:
Db          2 RPYIHPFQL 10


RESULT 8
P82325
ID   P82325      PRELIMINARY;      PRT;    12 AA.
AC   P82325;
DT   01-JUN-2000 (TrEMBLrel. 14, Created)
DT   01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Unknown protein from 2D-page of thylakoid (SPOT106) (Fragment).
OS   Pisum sativum (Garden pea).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
OX   NCBI_TaxID=3888;
RN   [1]
RP   SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC   STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX   MEDLINE=20181728; PubMed=10715320;
RA   Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA   Adamska I., van Wijk K.J.;
RT   "Proteomics of the chloroplast: systematic identification and
RT   targeting analysis of lumenal and peripheral thylakoid proteins.";
RL   Plant Cell 12:319-341(2000).
CC   -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR
CC       PERIPHERY.
CC   -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC   -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC       PROTEIN IS: 5.3, ITS MW IS: 18.2 KDA.
DR   GO; GO:0009507; C:chloroplast; IEA.
DR   GO; GO:0009579; C:thylakoid; IEA.
KW   Chloroplast; Thylakoid.
FT   NON_TER      12      12
SQ   SEQUENCE   12 AA;  1236 MW;  CEAC7ADC02633452 CRC64;

  Query Match             27.6%;  Score 27;  DB 10;  Length 12;
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  Best Local Similarity   62.5%;  Pred. No. 1.2e+03;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 VEKPDLQP 13
              | ||:| |
Db          5 VNKPELLP 12


RESULT 9
Q9UCI2
ID   Q9UCI2      PRELIMINARY;      PRT;    16 AA.
AC   Q9UCI2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Tropomyosin (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=93195352; PubMed=8450225;
RA   Das K.M., Dasgupta A., Mandal A., Geng X.;
RT   "Autoimmunity to cytoskeletal protein tropomyosin. A clue to the
RT   pathogenetic mechanism for ulcerative colitis.";
RL   J. Immunol. 150:2487-2493(1993).
SQ   SEQUENCE   16 AA;  1960 MW;  7A26C4941E0A335E CRC64;

  Query Match             27.6%;  Score 27;  DB 4;  Length 16;
  Best Local Similarity   38.5%;  Pred. No. 1.7e+03;
  Matches    5;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 DVEKPDLQPFQVQ 17
              | || ::|  |::
Db          4 DEEKMEIQEIQLK 16


RESULT 10
Q8MNX0
ID   Q8MNX0      PRELIMINARY;      PRT;    18 AA.
AC   Q8MNX0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Bombyx mori (Silk moth).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC   Bombycidae; Bombyx.
OX   NCBI_TaxID=7091;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RA   Eystathioy T., Swevers L., Iatrou K.;
RT   "The orphan nuclear receptors BmE75A, C and D from the silkmoth Bombyx
RT   mori: hormonal control and ovarian expression.";
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RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF332552; AAM43817.1; -.
KW   Hypothetical protein.
FT   NON_TER       1      1
FT   NON_TER      18     18
SQ   SEQUENCE   18 AA;  2012 MW;  072C6D18DFF0ED5E CRC64;

  Query Match             27.6%;  Score 27;  DB 5;  Length 18;
  Best Local Similarity   50.0%;  Pred. No. 1.9e+03;
  Matches    4;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 QPPDVEKP 9
              :||  |:|
Db          4 KPPSFEEP 11


RESULT 11
Q9S8G8
ID   Q9S8G8      PRELIMINARY;      PRT;    18 AA.
AC   Q9S8G8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   Proline-rich protein (Fragment).
OS   Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC   Psophocarpus.
OX   NCBI_TaxID=3891;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=95277008; PubMed=7757337;
RA   Esaka M., Hayakawa H.;
RT   "Specific secretion of proline-rich proteins by salt-adapted winged
RT   bean cells.";
RL   Plant Cell Physiol. 36:441-446(1995).
SQ   SEQUENCE   18 AA;  2252 MW;  4FD7D1DA18B5D94A CRC64;

  Query Match             27.6%;  Score 27;  DB 10;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.9e+03;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 PDVEKP 9
              | ||||
Db          9 PKVEKP 14


RESULT 12
Q9UEE2
ID   Q9UEE2      PRELIMINARY;      PRT;    13 AA.
AC   Q9UEE2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   ERGB transcription factor (Fragment).
GN   FLI1.
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OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Obata K., Hiraga H., Nojima T., Yoshida M.C., Abe S.;
RT   "Molecular analysis on the breakpoint region of a t(11:22)
RT   translocation in Ewing's sarcoma.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB012625; BAA32806.1; -.
FT   NON_TER       1      1
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1541 MW;  2C677798CB566AB7 CRC64;

  Query Match             26.5%;  Score 26;  DB 4;  Length 13;
  Best Local Similarity   30.0%;  Pred. No. 1.9e+03;
  Matches    3;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 EKPDLQPFQV 16
              ::|   |:|:
Db          2 QRPQPDPYQI 11


RESULT 13
Q9UWH3
ID   Q9UWH3      PRELIMINARY;      PRT;    15 AA.
AC   Q9UWH3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   Keto-valine-ferredoxin oxidoreductase beta-subunit, VOR beta
DE   (Fragment).
OS   Thermococcus litoralis.
OC   Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC   Thermococcus.
OX   NCBI_TaxID=2265;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=96146528; PubMed=8550513;
RA   Heider J., Mai X., Adams M.W.;
RT   "Characterization of 2-ketoisovalerate ferredoxin oxidoreductase, a
RT   new and reversible coenzyme A-dependent enzyme involved in peptide
RT   fermentation by hyperthermophilic archaea.";
RL   J. Bacteriol. 178:780-787(1996).
SQ   SEQUENCE   15 AA;  1740 MW;  5C0D6371E91D4C4F CRC64;

  Query Match             26.5%;  Score 26;  DB 1;  Length 15;
  Best Local Similarity   50.0%;  Pred. No. 2.2e+03;
  Matches    6;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 PPDVEKPDLQPF 14
              | ||:|    ||
Db          4 PADVKKRLTLPF 15


RESULT 14
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Q9TR14
ID   Q9TR14      PRELIMINARY;      PRT;    15 AA.
AC   Q9TR14;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   Troponin-T homolog/proteolysis CONDITIONING INDICATOR peptide
DE   (Fragment).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=96187584; PubMed=8611748;
RA   Nakai Y., Nishimura T., Shimizu M., Arai S.;
RT   "Effects of freezing on the proteolysis of beef during storage at 4
RT   degrees C.";
RL   Biosci. Biotechnol. Biochem. 59:2255-2258(1995).
SQ   SEQUENCE   15 AA;  1597 MW;  C98A5B44A79E4777 CRC64;

  Query Match             26.5%;  Score 26;  DB 6;  Length 15;
  Best Local Similarity   44.4%;  Pred. No. 2.2e+03;
  Matches    4;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 PPDVEKPDL 11
              ||  | |:::
Db          3 PPPAEVPEV 11


RESULT 15
Q9JK08
ID   Q9JK08      PRELIMINARY;      PRT;    17 AA.
AC   Q9JK08;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Fructose-1,6-bisphosphatase (EC 3.1.3.11) (Fragment).
GN   FBP2 OR FBPASE 2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=20237676; PubMed=10773464;
RA   Tillmann H., Stein S., Liehr T., Eschrich K.;
RT   "Structure and chromosomal localization of the human and mouse muscle
RT   fructose-1,6-bisphosphatase genes.";
RL   Gene 247:241-253(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RA   Stein S.;
RT   "Mouse liver fructose-1,6-Bisphosphatase: Gene structure,
```

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RT   transcriptional start point, chromosomal localization, cDNA cloning,
RT   characterization of the recombinant protein, and analysis of tissue-
RT   specific expression.";
RL   Arch. Biochem. Biophys. 0:0-0(0).
DR   EMBL; AJ243021; CAB90668.1; -.
DR   MGD; MGI:95491; Fbp2.
DR   GO; GO:0042132; F:fructose-bisphosphatase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
KW   Hydrolase.
FT   NON_TER       1      1
FT   NON_TER      17     17
SQ   SEQUENCE   17 AA;  1887 MW;  E2609FFD33922C8B CRC64;

  Query Match             26.5%;  Score 26;  DB 11;  Length 17;
  Best Local Similarity   53.8%;  Pred. No. 2.6e+03;
  Matches    7;  Conservative    1;  Mismatches    3;  Indels    2;  Gaps    1;

Qy          1 DQPPDVEKPDLQP 13
              |:|   ||  |||
Db          4 DEPS--EKDALQP 14


RESULT 16
P90402
ID   P90402      PRELIMINARY;      PRT;    17 AA.
AC   P90402;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Vpr protein.
GN   VPR.
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Z321B;
RX   MEDLINE=97225063; PubMed=9071436;
RA   Choi D.J., Dube S., Spicer T.P., Slade H.B., Jensen F.C., Poiesz B.J.;
RT   "HIV type 1 isolate Z321, the strain used to make a therapeutic HIV
RT   type 1 immunogen, is intersubtype recombinant.";
RL   AIDS Res. Hum. Retroviruses 13:357-361(1997).
DR   EMBL; U76035; AAB54106.1; -.
SQ   SEQUENCE   17 AA;  1969 MW;  58CA75563F4457C7 CRC64;

  Query Match             26.5%;  Score 26;  DB 15;  Length 17;
  Best Local Similarity   30.8%;  Pred. No. 2.6e+03;
  Matches    4;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DQPPDVEKPDLQP 13
              :| |: : |  :|
Db          2 EQAPEDQGPQREP 14


RESULT 17
Q9Q709
ID   Q9Q709      PRELIMINARY;      PRT;    17 AA.
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AC   Q9Q709;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Truncated Vpr.
GN   VPR.
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VI997;
RX   MEDLINE=20436917; PubMed=10983640;
RA   Janssens W., Laukkanen T., Salminen M.O., Carr J.K.,
RA   Van der Auwera G., Heyndrickx L., van der Groen G., McCutchan F.E.;
RT   "HIV-1 subtype H near-full length genome reference strains and
RT   analysis of subtype-H-containing inter-subtype recombinants.";
RL   AIDS 14:1533-1543(2000).
DR   EMBL; AF190128; AAF18410.1; -.
DR   InterPro; IPR000012; RetroV_VpR/X.
DR   Pfam; PF00522; VPR; 1.
KW   AIDS.
SQ   SEQUENCE   17 AA;  1992 MW;  58CA70F63F4457C7 CRC64;

  Query Match             26.5%;  Score 26;  DB 15;  Length 17;
  Best Local Similarity   30.8%;  Pred. No. 2.6e+03;
  Matches    4;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DQPPDVEKPDLQP 13
              :| |: : |  :|
Db          2 EQAPEDQGPQREP 14


RESULT 18
Q9X3E9
ID   Q9X3E9      PRELIMINARY;      PRT;    18 AA.
AC   Q9X3E9;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   Cytochrome b6/f complex subunit IV (Fragment).
GN   PETD.
OS   Prochlorococcus sp.
OC   Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC   Prochlorococcus.
OX   NCBI_TaxID=1220;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Urbach E., Chisholm S.W.;
RT   "Genetic diversity in Prochlorococcus populations flow cytometrically
RT   sorted from the Sargasso Sea and Gulf Stream.";
RL   Limnol. Oceanog. 43:1615-1630(1998).
DR   EMBL; AF070147; AAD20766.1; -.
FT   NON_TER      18     18
SQ   SEQUENCE   18 AA;  2029 MW;  EBF8A4E54FDCDE56 CRC64;

  Query Match             26.5%;  Score 26;  DB 2;  Length 18;
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  Best Local Similarity   41.7%;  Pred. No. 2.7e+03;
  Matches    5;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 PDVEKPDLQPFQ 15
              ||:  | |:  |
Db          7 PDLSDPKLRATQ 18


RESULT 19
Q9TWL5
ID   Q9TWL5      PRELIMINARY;      PRT;    18 AA.
AC   Q9TWL5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   24 kDa chymotrypsin-like enzyme (Fragment).
OS   Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC   Calliphoridae; Lucilia.
OX   NCBI_TaxID=7375;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=95219141; PubMed=7704304;
RA   Casu R.E., Pearson R.D., Jarmey J.M., Cadogan L.C., Riding G.A.,
RA   Tellam R.L.;
RT   "Excretory/secretory chymotrypsin from Lucilia cuprina: purification,
RT   enzymatic specificity and amino acid sequence deduced from mRNA.";
RL   Insect Mol. Biol. 3:201-211(1994).
DR   InterPro; IPR009003; Cys_Ser_trypsin.
SQ   SEQUENCE   18 AA;  2002 MW;  AC29200B9B184300 CRC64;

  Query Match             26.5%;  Score 26;  DB 5;  Length 18;
  Best Local Similarity   62.5%;  Pred. No. 2.7e+03;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          9 PDLQPFQV 16
              | | |:||
Db          9 PGLFPYQV 16


RESULT 20
P83061
ID   P83061      PRELIMINARY;      PRT;    17 AA.
AC   P83061;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Putative FK506-binding protein (FKBP) (Peptidyl-prolyl cis-trans
DE   isomerase) (PPIase) (EC 5.2.1.8) (Fragment).
OS   Spinacia oleracea (Spinach).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Caryophyllales; Amaranthaceae; Spinacia.
OX   NCBI_TaxID=3562;
RN   [1]
RP   SEQUENCE, AND SUBCELLULAR LOCATION.
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RA   Schubert M., Peterson U., Funk C., Haas B., Schroeder W.P.,
RA   Kieselbach T.;
RL   Submitted (JUL-2001) to Swiss-Prot.
CC   -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY
CC       SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC       PEPTIDE BONDS IN OLIGOPEPTIDES.
CC   -!- SUBCELLULAR LOCATION: CHLOROPLAST; WITHIN THE THYLAKOID LUMEN.
CC   -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
DR   GO; GO:0009507; C:chloroplast; IEA.
DR   GO; GO:0042027; F:cyclophilin-type peptidyl-prolyl cis-trans . . .; IEA.
DR   GO; GO:0004600; F:cyclophilin; IEA.
DR   GO; GO:0030051; F:FK506-sensitive peptidyl-prolyl cis-trans i. . .; IEA.
DR   GO; GO:0016853; F:isomerase activity; IEA.
DR   GO; GO:0006457; P:protein folding; IEA.
DR   InterPro; IPR001179; FKBP_PPIase.
KW   Isomerase; Rotamase; Chloroplast.
FT   NON_TER      17     17
SQ   SEQUENCE   17 AA;  1771 MW;  E2013F998EFBF908 CRC64;

  Query Match             26.0%;  Score 25.5;  DB 10;  Length 17;
  Best Local Similarity   66.7%;  Pred. No. 3.1e+03;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          3 PPDVEKPDL 11
              ||: ||| |
Db          4 PPE-EKPKL 11


RESULT 21
Q9UCT9
ID   Q9UCT9      PRELIMINARY;      PRT;    18 AA.
AC   Q9UCT9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   PRG=PROLINE-rich glycoprotein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=91373355; PubMed=1894623;
RA   Gillece-Castro B.L., Prakobphol A., Burlingame A.L., Leffler H.,
RA   Fisher S.J.;
RT   "Structure and bacterial receptor activity of a human salivary
RT   proline-rich glycoprotein.";
RL   J. Biol. Chem. 266:17358-17368(1991).
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0008368; F:Gram-negative bacterial binding; NAS.
DR   GO; GO:0009618; P:response to pathogenic bacteria; NAS.
FT   NON_TER      1      1
FT   NON_TER     18     18
SQ   SEQUENCE   18 AA;  1780 MW;  961F6FB0A83D2E40 CRC64;

  Query Match             25.5%;  Score 25;  DB 4;  Length 18;
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  Best Local Similarity   46.2%;  Pred. No. 3.9e+03;
  Matches    6;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          3 PPDVEKPDLQPFQ 15
              ||   ||:  | |
Db          5 PPRPGKPEGPPPQ 17


RESULT 22
Q9S618
ID   Q9S618      PRELIMINARY;      PRT;    11 AA.
AC   Q9S618;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   Cytochrome b6/f complex subunit IV (Fragment).
GN   PETD.
OS   Prochlorococcus sp.
OC   Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC   Prochlorococcus.
OX   NCBI_TaxID=1220;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Urbach E., Chisholm S.W.;
RT   "Genetic diversity in Prochlorococcus populations flow cytometrically
RT   sorted from the Sargasso Sea and Gulf Stream.";
RL   Limnol. Oceanog. 43:1615-1630(1998).
DR   EMBL; AF070132; AAD20740.1; -.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1297 MW;  5CC38013B7633337 CRC64;

  Query Match             24.5%;  Score 24;  DB 2;  Length 11;
  Best Local Similarity   66.7%;  Pred. No. 3.3e+03;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 VEKPDL 11
              ::||||
Db          4 LKKPDL 9


RESULT 23
P82328
ID   P82328      PRELIMINARY;      PRT;    12 AA.
AC   P82328;
DT   01-JUN-2000 (TrEMBLrel. 14, Created)
DT   01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Unknown protein from 2D-page of thylakoid lumen (SPOT110) (Fragment).
OS   Pisum sativum (Garden pea).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
OX   NCBI_TaxID=3888;
RN   [1]
RP   SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC   STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX   MEDLINE=20181728; PubMed=10715320;
```

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RA   Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA   Adamska I., van Wijk K.J.;
RT   "Proteomics of the chloroplast: systematic identification and
RT   targeting analysis of lumenal and peripheral thylakoid proteins.";
RL   Plant Cell 12:319-341(2000).
CC   -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC   -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC   -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC       PROTEIN IS: 6.0, ITS MW IS: 21.3 KDA.
DR   GO; GO:0009507; C:chloroplast; IEA.
DR   GO; GO:0009579; C:thylakoid; IEA.
KW   Chloroplast; Thylakoid.
FT   NON_TER      12     12
SQ   SEQUENCE   12 AA;  1264 MW;  96691CBC663B1B01 CRC64;

  Query Match             24.5%;  Score 24;  DB 10;  Length 12;
  Best Local Similarity   62.5%;  Pred. No. 3.6e+03;
  Matches    5;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 PDVEKPDL 11
              |  ||| |
Db          4 PTEEKPPL 11


RESULT 24
Q9R3R6
ID   Q9R3R6      PRELIMINARY;      PRT;    13 AA.
AC   Q9R3R6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   Cytochrome B6/F complex subunit IV (Fragment).
GN   PETD.
OS   Prochlorococcus sp.
OC   Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC   Prochlorococcus.
OX   NCBI_TaxID=1220;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Urbach E., Chisholm S.W.;
RT   "Genetic diversity in Prochlorococcus populations flow cytometrically
RT   sorted from the Sargasso Sea and Gulf Stream.";
RL   Limnol. Oceanog. 43:1615-1630(1998).
DR   EMBL; AF070222; AAD23275.1; -.
DR   EMBL; AF070221; AAD23273.1; -.
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1522 MW;  4CDE4CC38013B763 CRC64;

  Query Match             24.5%;  Score 24;  DB 2;  Length 13;
  Best Local Similarity   66.7%;  Pred. No. 3.9e+03;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 VEKPDL 11
              ::||||
Db          4 LKKPDL 9
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RESULT 25
Q9LB06
ID   Q9LB06      PRELIMINARY;      PRT;    17 AA.
AC   Q9LB06;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   Cytochrome b6/f complex subunit IV (Fragment).
GN   PETD.
OS   Prochlorococcus sp.
OC   Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC   Prochlorococcus.
OX   NCBI_TaxID=1220;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Urbach E., Chisholm S.W.;
RT   "Genetic diversity in Prochlorococcus populations flow cytometrically
RT   sorted from the Sargasso Sea and Gulf Stream.";
RL   Limnol. Oceanog. 43:1615-1630(1998).
DR   EMBL; AF070156; AAD23199.2; -.
FT   NON_TER       1      1
FT   NON_TER      17     17
SQ   SEQUENCE   17 AA;  1904 MW;  CCEB69C5A202E54F CRC64;

  Query Match             24.5%;  Score 24;  DB 2;  Length 17;
  Best Local Similarity   44.4%;  Pred. No. 5.2e+03;
  Matches    4;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 PDVEKPDLQ 12
              ||:  | |:
Db          3 PDLSDPKLR 11


RESULT 26
O67971
ID   O67971      PRELIMINARY;      PRT;    18 AA.
AC   O67971;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   B6/f complex subunit IV (Fragment).
GN   PETD.
OS   Synechococcus sp. (strain WH8103).
OC   Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX   NCBI_TaxID=29410;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WH8103;
RX   MEDLINE=98123172; PubMed=9452521;
RA   Urbach E., Scanlan D.J., Distel D.L., Waterbury J.B., Chisholm S.W.;
RT   "Rapid diversification of marine picophytoplankton with dissimilar
RT   light-harvesting structures inferred from sequences of Prochlorococcus
RT   and Synechococcus (Cyanobacteria).";
RL   J. Mol. Evol. 46:188-201(1998).
DR   EMBL; AF001492; AAC05631.1; -.
FT   NON_TER      18     18
SQ   SEQUENCE   18 AA;  2098 MW;  C205CA0BB21CDE4C CRC64;
```

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  Query Match             24.5%;  Score 24;  DB 2;  Length 18;
  Best Local Similarity   66.7%;  Pred. No. 5.6e+03;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 VEKPDL 11
              ::||||
Db          4 LKKPDL 9


RESULT 27
Q9UCS8
ID   Q9UCS8      PRELIMINARY;      PRT;     9 AA.
AC   Q9UCS8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Apolipoprotein A-I (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92075698; PubMed=1742316;
RA   Ehnholm C., Bozas S.E., Tenkanen H., Kirszbaum L., Metso J.,
RA   Murphy B., Walker I.D.;
RT   "The apolipoprotein A-I binding protein of placenta and the SP-40,40
RT   protein of human blood are different proteins which both bind to
RT   apolipoprotein A-I.";
RL   Biochim. Biophys. Acta 1086:255-260(1991).
DR   GO; GO:0005576; C:extracellular; ISS.
DR   GO; GO:0005319; F:lipid transporter activity; NAS.
DR   GO; GO:0008203; P:cholesterol metabolism; ISS.
DR   GO; GO:0006869; P:lipid transport; ISS.
FT   NON_TER       1      1
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  981 MW;  7FE37775A6C7776B CRC64;

  Query Match             24.0%;  Score 23.5;  DB 4;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 1e+06;
  Matches    5;  Conservative    1;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 DQPPDVEKPD 10
              |:||    ||
Db          1 DEPPQ-SPPD 9


RESULT 28
Q9R735
ID   Q9R735      PRELIMINARY;      PRT;     9 AA.
AC   Q9R735;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   FkbA protein (Fragment).
GN   FKBA.
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```
OS   Streptomyces chrysomallus.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1899;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94341259; PubMed=8062824;
RA   Pahl A., Keller U.;
RT   "Streptomyces chrysomallus FKBP-33 is a novel immunophilin consisting
RT   of two FK506-binding domains with its gene transcriptionally coupled
RT   to the FKBP-12 gene.";
RL   EMBO J. 13:3472-3480(1994).
DR   EMBL; Z34523; CAA84282.1; -.
FT   NON_TER       9       9
SQ   SEQUENCE   9 AA;  1047 MW;  9A8BCB07633B1045 CRC64;

  Query Match             23.5%;  Score 23;  DB 2;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 VEKPDL 11
              :|||::
Db          3 IEKPEV 8


RESULT 29
P81715
ID   P81715      PRELIMINARY;      PRT;    14 AA.
AC   P81715;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Leupeptin-inactivating enzyme (EC 3.4.24.-) (LIE) (Fragment).
OS   Streptomyces exfoliatus (Streptomyces hydrogenans).
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1905;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=SMF13;
RX   PubMed=9531495;
RA   Kim I.S., Kim Y.B., Lee K.J.;
RT   "Characterization of the leupeptin-inactivating enzyme from
RT   Streptomyces exfoliatus SMF13 which produces leupeptin.";
RL   Biochem. J. 331:539-545(1998).
CC   -!- FUNCTION: A LEUCINE-SPECIFIC METALLOPROTEASE THAT PLAYS A ROLE IN
CC       CONTROLLING THE AMOUNT OF LEUPEPTIN DURING COLONY DEVELOPMENT.
CC       OPTIMUM PH IS 9.0 AND TEMPERATURE IS 40 DEGREES CELSIUS.
CC   -!- FUNCTION: DEGRADES LEUPEPTIN INTO THREE COMPONENTS, ACETYL-
CC       LEUCINE, LEUCINE AND ARGININAL.
CC   -!- CATALYTIC ACTIVITY: HAS A STRICT PREFERENCE FOR LEUCINE AT THE P1
CC       SITE.
CC   -!- ENZYME REGULATION: ACTIVITY IS INHIBITED BY METALLOPROTEASE
CC       INHIBITORS AND ACTIVATED BY MG2+ AND CA2+.
CC   -!- SUBUNIT: MONOMER.
CC   -!- SUBCELLULAR LOCATION: SECRETED.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
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DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
KW   Hydrolase; Metalloprotease.
FT   NON_TER      14      14
SQ   SEQUENCE   14 AA;  1373 MW;  14D627940C973260 CRC64;

  Query Match             23.5%;  Score 23;  DB 2;  Length 14;
  Best Local Similarity   75.0%;  Pred. No. 6.1e+03;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 PPDV 6
              |||:
Db          4 PPDI 7


RESULT 30
P97135
ID   P97135      PRELIMINARY;      PRT;    17 AA.
AC   P97135;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   GyrA protein (Fragment).
GN   GYRA.
OS   Mycobacterium tuberculosis.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX   NCBI_TaxID=1773;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=H37Ra;
RX   MEDLINE=95072534; PubMed=7981652;
RA   Madhusudan K., Ramesh V., Nagaraja V.;
RT   "Molecular cloning of gyrA and gyrB genes of Mycobacterium
RT   tuberculosis:analysis of nucleotide sequence.";
RL   Biochem. Mol. Biol. Int. 33:651-660(1994).
DR   EMBL; X78888; CAA55487.1; -.
FT   NON_TER      17      17
SQ   SEQUENCE   17 AA;  1916 MW;  EF0B750A36E365AE CRC64;

  Query Match             23.5%;  Score 23;  DB 2;  Length 17;
  Best Local Similarity   36.4%;  Pred. No. 7.5e+03;
  Matches    4;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 PPDVEKPDLQP 13
              |||     ::|
Db          7 PPDDSLDRIEP 17


RESULT 31
Q7YMC5
ID   Q7YMC5      PRELIMINARY;      PRT;    18 AA.
AC   Q7YMC5;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   PsbT (Fragment).
GN   PSBT.
```

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OS   Pogonatum subulatum.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC   Polytrichopsida; Polytrichales; Polytrichaceae; Pogonatum.
OX   NCBI_TaxID=172817;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Quandt D.;
RT   "The systematic position of Pulchrinodus inflatus (Pulchrinodaceae,
RT   Bryopsida) based on molecular data.";
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY122276; AAM88440.1; -.
KW   Chloroplast.
FT   NON_TER       1      1
SQ   SEQUENCE   18 AA;  2184 MW;  24635A05ED23942E CRC64;

  Query Match             23.5%;  Score 23;  DB 8;  Length 18;
  Best Local Similarity   50.0%;  Pred. No. 7.9e+03;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QPPDVE 7
              :|| :|
Db          8 EPPKIE 13


RESULT 32
Q9L5W6
ID   Q9L5W6      PRELIMINARY;      PRT;    10 AA.
AC   Q9L5W6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   RplA (Fragment).
GN   RPLA.
OS   Liberibacter africanus (subsp. capensis).
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Rhizobiaceae; Candidatus Liberibacter.
OX   NCBI_TaxID=119494;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Garnier M., Jagoueix-Eveillard S., Cronje P., Le Roux H., Bove J.;
RT   "Genomic characterization of a Liberibacter present in an ornamental
RT   rutaceous tree, Calodendrum capense, in the western Cape province of
RT   South Africa. Proposal of 'candidatus Liberibacter africanus
RT   subspecies capensis'.";
RL   Int. J. Syst. Evol. Microbiol. 0:0-0(2000).
DR   EMBL; AF248498; AAF68451.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   10 AA;  1094 MW;  C42894D5A5B72AB2 CRC64;

  Query Match             22.4%;  Score 22;  DB 2;  Length 10;
  Best Local Similarity   55.6%;  Pred. No. 6.1e+03;
  Matches    5;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          8 KPDLQPFQV 16
              | ||  | |
Db          2 KVDLSSFSV 10
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RESULT 33
Q8HYM4
ID   Q8HYM4      PRELIMINARY;      PRT;    11 AA.
AC   Q8HYM4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Coagulation factor IX (Fragment).
GN   F9.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Susott E.E., Rollo W.A., Venta P.J., Ewart S.L.;
RT   "Characterization of 8 Feline Type I Markers.";
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF459805; AAO15586.1; -.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1169 MW;  9C8E7EFCA05B02CA CRC64;

  Query Match             22.4%;  Score 22;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 PDVE 7
              ||||
Db          3 PDVE 6


RESULT 34
Q9R1U3
ID   Q9R1U3      PRELIMINARY;      PRT;    14 AA.
AC   Q9R1U3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   R-ras GTPase activating protein (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RA   Iwashita S.;
RT   "5'-flanking region of R-ras GTPase activating protein.";
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB021982; BAA81903.1; -.
FT   NON_TER      14     14
SQ   SEQUENCE   14 AA;  1594 MW;  3C91E28A0C8E3E28 CRC64;

  Query Match             22.4%;  Score 22;  DB 11;  Length 14;
```

```
  Best Local Similarity   50.0%;  Pred. No. 8.7e+03;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 VEKPDLQPFQ 15
              ||:  |: ||
Db          3 VEEEGLRVFQ 12


RESULT 35
O69142
ID   O69142      PRELIMINARY;      PRT;    15 AA.
AC   O69142;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Protein SIC (Fragment).
GN   SIC.
OS   Streptococcus pyogenes.
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC   Streptococcus.
OX   NCBI_TaxID=1314;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AP1;
RX   MEDLINE=98298075; PubMed=9632622;
RA   Berge A., Rasmussen M., Bjorck L.;
RT   "Identification of an insertion sequence located in a region encoding
RT   virulence factors of Streptococcus pyogenes.";
RL   Infect. Immun. 66:3449-3453(1998).
DR   EMBL; AF064540; AAC38769.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   15 AA;  1552 MW;  87655FEF847401FF CRC64;

  Query Match             22.4%;  Score 22;  DB 2;  Length 15;
  Best Local Similarity   42.9%;  Pred. No. 9.4e+03;
  Matches    3;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 KPDLQPF 14
              || : |:
Db          4 KPSVTPY 10


RESULT 36
Q08936
ID   Q08936      PRELIMINARY;      PRT;    15 AA.
AC   Q08936;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Chloroplast 29 kDa ribonucleoprotein A (CP29A) (Fragment).
OS   Nicotiana tabacum (Common tobacco).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Solanales; Solanaceae; Nicotiana.
OX   NCBI_TaxID=4097;
RN   [1]
RP   SEQUENCE.
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RC   TISSUE=LEAF;
RA   Ye L., Li Y., Fukami-Kobayashi F., Go M., Konishi T., Watanbe A.,
RA   Sugiura M.;
RL   Nucleic Acids Res. 19:6485-6490(1994).
CC   -!- FUNCTION: COULD BE INVOLVED IN SPLICING AND/OR PROCESSING OF
CC       CHLOROPLAST RNA'S.
CC   -!- SUBCELLULAR LOCATION: CHLOROPLAST.
DR   GO; GO:0009507; C:chloroplast; IEA.
DR   GO; GO:0030529; C:ribonucleoprotein complex; IEA.
KW   Ribonucleoprotein; Chloroplast.
FT   NON_TER       1      1
FT   NON_TER      15     15
SQ   SEQUENCE   15 AA;  1682 MW;  C97821104B9756C8 CRC64;

  Query Match             22.4%;  Score 22;  DB 10;  Length 15;
  Best Local Similarity   71.4%;  Pred. No. 9.4e+03;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DQPPDVE 7
              ||  ||| 
Db          7 DQIEDVE 13


RESULT 37
Q9QVL2
ID   Q9QVL2      PRELIMINARY;      PRT;    16 AA.
AC   Q9QVL2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   MEPRIN=METALLOENDOPEPTIDASE (Fragment).
OS   Mus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10095;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=91363409; PubMed=1888759;
RA   Flannery A.V., Macadam G.C., Beynon R.J.;
RT   "Immunological characterisation of different meprin species in mice.";
RL   Biochim. Biophys. Acta 1079:119-122(1991).
FT   NON_TER       1      1
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1922 MW;  B0379F6803B42FAD CRC64;

  Query Match             22.4%;  Score 22;  DB 11;  Length 16;
  Best Local Similarity   33.3%;  Pred. No. 1e+04;
  Matches    3;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 DLQPFQVQS 18
              | :|:: :| 
Db          2 DFKPYEGES 10


RESULT 38
Q9EUP4
ID   Q9EUP4      PRELIMINARY;      PRT;    17 AA.
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AC   Q9EUP4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Cell division associated protein (Fragment).
GN   DIVIVA.
OS   Thermus thermophilus.
OC   Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC   Thermus.
OX   NCBI_TaxID=274;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=KT8;
RA   Spada S., Gibert Y., Pembroke J.T., Wall J.G.;
RT   "Cloning and characterisation of the ylmE homologue of Thermus
RT   thermophilus.";
RL   DNA Seq. 11:5007-5014(2001).
DR   EMBL; AJ297409; CAC21427.1; -.
FT   NON_TER      17     17
SQ   SEQUENCE   17 AA;  2084 MW;  0C642E1D509D87E3 CRC64;

  Query Match             22.4%;  Score 22;  DB 2;  Length 17;
  Best Local Similarity   50.0%;  Pred. No. 1.1e+04;
  Matches    4;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 DLQPFQVQ 17
                || |  |:
Db          2 DLSPLDVR 9


RESULT 39
O46667
ID   O46667      PRELIMINARY;      PRT;    17 AA.
AC   O46667;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Glucose-6-phosphate dehydrogenase (Fragment).
GN   G6PD.
OS   Macropus robustus robustus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX   NCBI_TaxID=35580;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97224585; PubMed=9060417;
RA   Loebel D.A., Johnston P.G.;
RT   "Analysis of the intron-exon structure of the G6PD gene of the
RT   wallaroo (Macropus robustus) by polymerase chain reaction.";
RL   Mamm. Genome 8:146-147(1997).
DR   EMBL; U53779; AAC48792.2; -.
DR   EMBL; U53778; AAC48792.2; JOINED.
DR   GO; GO:0004345; F:glucose-6-phosphate 1-dehydrogenase activity; IEA.
DR   GO; GO:0006006; P:glucose metabolism; IEA.
DR   InterPro; IPR001282; G6PD.
DR   Pfam; PF02781; G6PD_C; 1.
FT   NON_TER      1      1
```

```
FT   NON_TER       17      17
SQ   SEQUENCE   17 AA;  2039 MW;  3A5B76F61F908B21 CRC64;

  Query Match             22.4%;  Score 22;  DB 6;  Length 17;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+04;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 DVEKPD 10
              ||: ||
Db         12 DVKLPD 17


RESULT 40
Q95M99
ID   Q95M99      PRELIMINARY;      PRT;    17 AA.
AC   Q95M99;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypoxanthine guanine phosphoribosyltransferase 1 (Fragment).
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21314992; PubMed=11421942;
RA   Shubitowski D.M., Venta P.J., Douglass C.L., Zhou R.-X., Ewart S.L.;
RT   "Polymorphism identification within 50 equine gene-specific sequence
RT   tagged sites.";
RL   Anim. Genet. 32:78-78(2001).
DR   EMBL; AY008794; AAG40103.1; -.
DR   GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
KW   Glycosyltransferase; Transferase.
FT   NON_TER       1       1
FT   NON_TER      17      17
SQ   SEQUENCE   17 AA;  1973 MW;  893D20A6378F3311 CRC64;

  Query Match             22.4%;  Score 22;  DB 6;  Length 17;
  Best Local Similarity   33.3%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          8 KPDLQPFQV 16
              :||   |::
Db          5 RPDFVGFEI 13


RESULT 41
Q9QVC6
ID   Q9QVC6      PRELIMINARY;      PRT;    17 AA.
AC   Q9QVC6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   DW85 protein (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92291078; PubMed=1601872;
RA   Subramaniam V.N., bin Mohd Yusoff A.R., Wong S.H., Lim G.B., Chew M.,
RA   Hong W.;
RT   "Biochemical fractionation and characterization of proteins from
RT   Golgi-enriched membranes.";
RL   J. Biol. Chem. 267:12016-12021(1992).
FT   NON_TER      17     17
SQ   SEQUENCE   17 AA;  1949 MW;  BC939B267EF49CB7 CRC64;

  Query Match             22.4%;  Score 22;  DB 11;  Length 17;
  Best Local Similarity   40.0%;  Pred. No. 1.1e+04;
  Matches    4;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DQPPDVEKPD 10
              | | |  : |
Db          3 DYPEDXSQSD 12


RESULT 42
Q9QVC2
ID   Q9QVC2      PRELIMINARY;      PRT;    17 AA.
AC   Q9QVC2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Kallikrein light chain N-terminus (Fragment).
OS   Rattus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10118;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92329502; PubMed=1320938;
RA   Wang C., Tang C.Q., Zhou G.X., Chao L., Chao J.;
RT   "Biochemical characterization and substrate specificity of rat
RT   prostate kallikrein (S3): comparison with tissue kallikrein, tonin and
RT   T-kininogenase.";
RL   Biochim. Biophys. Acta 1121:309-316(1992).
DR   HSSP; P36368; 1AO5.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
FT   NON_TER       1      1
FT   NON_TER      17     17
SQ   SEQUENCE   17 AA;  1852 MW;  A403B510DF5C096D CRC64;

  Query Match             22.4%;  Score 22;  DB 11;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 1.1e+04;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 QPFQV 16
              ||:||
Db         12 QPWQV 16
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RESULT 43
Q919B0
ID   Q919B0      PRELIMINARY;      PRT;    17 AA.
AC   Q919B0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   E7 protein (Fragment).
GN   E7.
OS   Human papillomavirus type 16.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Papillomavirus.
OX   NCBI_TaxID=10581;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HPV16E6CC14;
RA   Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT   "Sequence variation and physical state of human papillomavirus type 16
RT   cervical cancer isolates from Australia and New Caledonia.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF404705; AAL01367.1; -.
FT   NON_TER      17     17
SQ   SEQUENCE   17 AA;  1998 MW;  4471DB6BF776889B CRC64;

  Query Match             22.4%;  Score 22;  DB 12;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 DLQP 13
              ||||
Db         14 DLQP 17


RESULT 44
Q56610
ID   Q56610      PRELIMINARY;      PRT;    18 AA.
AC   Q56610;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   AccA (Fragment).
GN   ACCA.
OS   Vibrio cholerae.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC   Vibrionaceae; Vibrio.
OX   NCBI_TaxID=666;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C6706;
RX   MEDLINE=97074686; PubMed=8917113;
RA   Franco A., Peir-En Y., Johnson J., Barry E.M., Guerra H., Maurer R.,
RA   Morris J.G.;
RT   "Cloning and characterization of dnaE, encoding the catalytic subunit
RT   of replicative DNA polymerase III, from Vibrio cholerae strain
RT   C6706.";
RL   Gene 175:281-283(1996).
DR   EMBL; U30472; AAC44579.1; -.
```

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FT   NON_TER       18      18
SQ   SEQUENCE   18 AA;  2153 MW;  18EBCDAD212842EF CRC64;

  Query Match             22.4%;  Score 22;  DB 2;  Length 18;
  Best Local Similarity   80.0%;  Pred. No. 1.1e+04;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 DVEKP 9
              | |||
Db          7 DFEKP 11


RESULT 45
Q9P0M3
ID   Q9P0M3      PRELIMINARY;      PRT;    18 AA.
AC   Q9P0M3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   Polymyositis/scleroderma autoantigen 2 (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bliskovsky V., Miller M., Mock B.;
RT   "Structure and localization of mouse PM-Scl genes.";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF152839; AAF73199.1; -.
FT   NON_TER       18      18
SQ   SEQUENCE   18 AA;  2025 MW;  A1F292BC77872D67 CRC64;

  Query Match             22.4%;  Score 22;  DB 4;  Length 18;
  Best Local Similarity   42.9%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 PPDVEKP 9
              ||   :|
Db          3 PPSTREP 9


RESULT 46
Q96C65
ID   Q96C65      PRELIMINARY;      PRT;    18 AA.
AC   Q96C65;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
```

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RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC014643; AAH14643.1; -.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   18 AA;  2105 MW;  3874A0D25D91AC9C CRC64;

  Query Match             22.4%;  Score 22;  DB 4;  Length 18;
  Best Local Similarity   44.4%;  Pred. No. 1.1e+04;
  Matches    4;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 EKPDLQPFQ 15
              |   |:||:
Db          7 ELESLRPFE 15


RESULT 47
Q9WTP8
ID   Q9WTP8      PRELIMINARY;      PRT;    18 AA.
AC   Q9WTP8;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   R-ras GTPase activating protein (Fragment).
GN   R-RAS GAP.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Spraque-Dawley;
RA   Iwashita S., Kobayashi M.;
RT   "NGF-mediated downregulation of R-ras GAP expression.";
RL   Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB020479; BAA78368.1; -.
FT   NON_TER      18     18
SQ   SEQUENCE   18 AA;  2104 MW;  6BC3355FDC91E28A CRC64;

  Query Match             22.4%;  Score 22;  DB 11;  Length 18;
  Best Local Similarity   50.0%;  Pred. No. 1.1e+04;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 VEKPDLQPFQ 15
              ||:  |: ||
Db          3 VEEEGLRVFQ 12


RESULT 48
Q919D5
ID   Q919D5      PRELIMINARY;      PRT;    18 AA.
AC   Q919D5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   E7 protein (Fragment).
GN   E7.
```

```
OS   Human papillomavirus type 16.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Papillomavirus.
OX   NCBI_TaxID=10581;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HPV16E6CC1;
RA   Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT   "Sequence variation and physical state of human papillomavirus type 16
RT   cervical cancer isolates from Australia and New Caledonia.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF404692; AAL01341.1; -.
FT   NON_TER      18     18
SQ   SEQUENCE   18 AA;  2127 MW;  A76471DB6BF77688 CRC64;

  Query Match             22.4%;  Score 22;  DB 12;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 DLQP 13
              ||||
Db         14 DLQP 17


RESULT 49
Q919B3
ID   Q919B3      PRELIMINARY;      PRT;    18 AA.
AC   Q919B3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   E7 protein (Fragment).
GN   E7.
OS   Human papillomavirus type 16.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Papillomavirus.
OX   NCBI_TaxID=10581;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HPV16E6CC12;
RA   Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT   "Sequence variation and physical state of human papillomavirus type 16
RT   cervical cancer isolates from Australia and New Caledonia.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF404703; AAL01364.1; -.
FT   NON_TER      18     18
SQ   SEQUENCE   18 AA;  2127 MW;  A76471DB6BF77688 CRC64;

  Query Match             22.4%;  Score 22;  DB 12;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 DLQP 13
              ||||
Db         14 DLQP 17
```

```
RESULT 50
Q919B5
ID   Q919B5      PRELIMINARY;      PRT;    18 AA.
AC   Q919B5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   E7 protein (Fragment).
GN   E7.
OS   Human papillomavirus type 16.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Papillomavirus.
OX   NCBI_TaxID=10581;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HPV16E6CC11;
RA   Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT   "Sequence variation and physical state of human papillomavirus type 16
RT   cervical cancer isolates from Australia and New Caledonia.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF404702; AAL01362.1; -.
FT   NON_TER      18     18
SQ   SEQUENCE   18 AA;  2127 MW;  A76471DB6BF77688 CRC64;

  Query Match             22.4%;  Score 22;  DB 12;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 DLQP 13
              ||||
Db         14 DLQP 17


Search completed: July  4, 2004, 04:45:29
Job time : 33.6269 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:33:26 ; Search time 6.1791 Seconds
(without alignments)
151.683 Million cell updates/sec

Title: US-09-641-802-3
Perfect score: 98
Sequence: 1 DQPPDVEKPDLQPFQVQS 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 952

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	31	31.6	15	1	MK1_PALPR	P80408 palomena pr
2	31	31.6	15	1	MK2A_PALPR	P80409 palomena pr
3	31	31.6	16	1	MK2B_PALPR	P80410 palomena pr
4	31	31.6	16	1	MK3_PALPR	P80411 palomena pr
5	30	30.6	10	1	URE3_MORMO	P17339 morganella
6	23	23.5	9	1	COXE_THUOB	P80975 thunnus obe
7	22	22.4	12	1	PPK4_PERAM	P82619 periplaneta
8	22	22.4	12	1	TKN2_KASMA	P08614 kassina mac
9	22	22.4	16	1	IBP4_PIG	P24854 sus scrofa
10	21	21.4	7	1	UF04_MOUSE	P38642 mus musculu
11	21	21.4	12	1	TKN1_KASMA	P08613 kassina mac
12	21	21.4	15	1	VORA_METTM	P80907 methanobact
13	20	20.4	10	1	SLAP_BACTG	P49325 bacillus th
14	20	20.4	10	1	UPA2_HUMAN	P30088 homo sapien
15	20	20.4	11	1	MORN_HUMAN	P01163 homo sapien
16	20	20.4	12	1	XYLA_STRVN	P14405 streptomyce
17	20	20.4	13	1	ACT7_SOYBN	P15987 glycine max

18	20	20.4	13	1	BRK_PARID	P42717 parapolybia
19	20	20.4	13	1	ECDE_LYMDI	P80941 lymantria d
20	20	20.4	17	1	ACT6_SOYBN	P15986 glycine max
21	20	20.4	17	1	PSBL_SYNVU	P12241 synechococc
22	20	20.4	17	1	VESP_VESMC	P57672 vespula mac
23	20	20.4	18	1	FIBA_LAMGL	P14454 lama glama
24	19.5	19.9	11	1	BPP3_BOTIN	P30423 bothrops in
25	19.5	19.9	11	1	BPP4_BOTIN	P30424 bothrops in
26	19	19.4	8	1	AL12_CARMA	P81815 carcinus ma
27	19	19.4	9	1	KNL3_BOMVA	P83058 bombina var
28	19	19.4	10	1	FARP_LOCMI	P38553 locusta mig
29	19	19.4	11	1	BRK_MEGFL	P12797 megascolia
30	19	19.4	12	1	TKN_KASSE	P08611 kassina sen
31	19	19.4	13	1	ODPA_CANFA	P49823 canis famil
32	19	19.4	17	1	SRY_URSAR	P36396 ursus arcto
33	18.5	18.9	11	1	BPPB_AGKHA	P01021 agkistrodon
34	18	18.4	9	1	LMT3_LOCMI	P41489 locusta mig
35	18	18.4	10	1	FAR6_PANRE	P82660 panagrellus
36	18	18.4	12	1	FARI_CALVO	P41869 calliphora
37	18	18.4	12	1	HS9A_RAT	P82995 rattus norv
38	18	18.4	13	1	EP65_HUMAN	P54963 homo sapien
39	18	18.4	13	1	PEDI_HYDAT	P80578 hydra atten
40	18	18.4	13	1	TY13_PHYRO	P04096 phyllomedus
41	18	18.4	14	1	MARI_ALTSP	P29399 alteromonas
42	18	18.4	15	1	HS11_PINPS	P81083 pinus pinas
43	18	18.4	15	1	PSAO_CUCSA	P42052 cucumis sat
44	18	18.4	15	1	UC23_MAIZE	P80629 zea mays (m
45	18	18.4	16	1	LPK1_LOCMI	P20404 locusta mig
46	18	18.4	18	1	LCTN_LAMGL	P83315 lama glama
47	17	17.3	10	1	BPP2_BOTJA	P01022 bothrops ja
48	17	17.3	10	1	BPP8_BOTIN	P30426 bothrops in
49	17	17.3	11	1	EFG_CLOPA	P81350 clostridium
50	17	17.3	11	1	RRPL_CHAV	P13179 chandipura
51	17	17.3	11	1	TKNA_GADMO	P28498 gadus morhu
52	17	17.3	12	1	FIF1_SARBU	P83349 sarcophaga
53	17	17.3	12	1	PPK4_PERFU	P82690 periplaneta
54	17	17.3	13	1	BPP1_BOTJA	P01020 bothrops ja
55	17	17.3	13	1	EI21_LITRU	P82097 litoria rub
56	17	17.3	13	1	EI22_LITRU	P82098 litoria rub
57	17	17.3	13	1	SODM_CANFA	P54712 canis famil
58	17	17.3	13	1	YPE2_LACLC	P42021 lactococcus
59	17	17.3	14	1	SODN_STRGR	P80732 streptomyce
60	17	17.3	14	1	TAT_HV1Z8	P12511 human immun
61	17	17.3	15	1	AF1L_MALPA	P83141 malva parvi
62	17	17.3	15	1	PRP_MYCBO	P80149 mycobacteri
63	17	17.3	15	1	RS6_BACST	P59682 bacillus st
64	17	17.3	15	1	UBL1_MONDO	P50103 monodelphis
65	17	17.3	15	1	UP02_METAN	P83439 metarhizium
66	17	17.3	16	1	AF1S_MALPA	P83140 malva parvi
67	17	17.3	17	1	A45K_MYCBO	P80069 mycobacteri
68	17	17.3	17	1	APID_BOMPA	P81464 bombus pasc
69	17	17.3	17	1	EFG_THEAQ	Q01697 thermus aqu
70	17	17.3	18	1	SODM_MYCHA	P80582 mycobacteri
71	16.5	16.8	11	1	BPP_AGKHP	P04562 agkistrodon
72	16	16.3	7	1	LANC_CARUI	P36960 carnobacter
73	16	16.3	8	1	PPK3_PERAM	P82618 periplaneta
74	16	16.3	9	1	ULAH_HUMAN	P31934 homo sapien

75	16	16.3	10	1	GON1_ALLMI	P37041	alligator m
76	16	16.3	11	1	TKN1_UPERU	P08612	uperoleia r
77	16	16.3	11	1	TKNA_RANRI	P29207	rana ridibu
78	16	16.3	11	1	TKND_RANCA	P22691	rana catesb
79	16	16.3	13	1	ADFB_TENMO	P83109	tenebrio mo
80	16	16.3	13	1	BLAC_STRGR	P81173	streptomyce
81	16	16.3	14	1	ANGT_HORSE	P01016	equus cabal
82	16	16.3	14	1	TAT_HV1W2	P12509	human immun
83	16	16.3	15	1	COXJ_THUOB	P80979	thunnus obe
84	16	16.3	15	1	PDGB_PIG	P20034	sus scrofa
85	16	16.3	15	1	PH2_PERAM	P82695	periplaneta
86	16	16.3	15	1	SODM_STRGR	P80733	streptomyce
87	16	16.3	16	1	CXAB_CONPE	P50985	conus penna
88	16	16.3	16	1	FOR1_MYRGU	P81438	myrmecia gu
89	16	16.3	18	1	CPAX_BOVIN	P22779	bos taurus
90	16	16.3	18	1	FIBA_CAMDR	P14444	camelus dro
91	16	16.3	18	1	FIXA_RHILE	P14313	rhizobium l
92	16	16.3	18	1	HEMH_THETS	P80155	theromyzon
93	16	16.3	18	1	RL23_HALCU	P05975	halobacteri
94	16	16.3	18	1	TKN2_SCYCA	P08609	scyliorhinu
95	15	15.3	7	1	TPFY_PACDA	P83455	pachymedusa
96	15	15.3	8	1	ANG2_BOTJA	Q10582	bothrops ja
97	15	15.3	8	1	B44K_PORGI	P81886	porphyromon
98	15	15.3	8	1	UPA1_HUMAN	P30087	homo sapien
99	15	15.3	9	1	AL10_CARMA	P81813	carcinus ma
100	15	15.3	9	1	FRF1_SARBU	P83350	sarcophaga

ALIGNMENTS

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RESULT 1
MK1_PALPR
ID   MK1_PALPR      STANDARD;      PRT;    15 AA.
AC   P80408;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Metalnikowin I.
OS   Palomena prasina (Green shield bug).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
OC   Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;
OC   Palomena.
OX   NCBI_TaxID=55431;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Hemolymph;
RA   Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
RT   "The inducible antibacterial peptides of the hemipteran insect
RT   Palomena prasina: identification of a unique family of proline-rich
RT   peptides and of a novel insect defensin.";
RL   J. Insect Physiol. 42:81-89(1996).
CC   -!- FUNCTION: Antibacterial peptide active against Gram-negative
CC       bacteria.
CC   -!- INDUCTION: By bacterial infection.
KW   Antibiotic; Insect immunity.
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SQ   SEQUENCE   15 AA;  1838 MW;  21407E663CE46299 CRC64;

  Query Match             31.6%;  Score 31;  DB 1;  Length 15;
  Best Local Similarity   62.5%;  Pred. No. 67;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 VEKPDLQP 13
              |:||| :|
Db          1 VDKPDYRP 8


RESULT 2
MK2A_PALPR
ID   MK2A_PALPR     STANDARD;      PRT;    15 AA.
AC   P80409;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Metalnikowin IIA.
OS   Palomena prasina (Green shield bug).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
OC   Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;
OC   Palomena.
OX   NCBI_TaxID=55431;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Hemolymph;
RA   Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
RT   "The inducible antibacterial peptides of the hemipteran insect
RT   Palomena prasina: identification of a unique family of proline-rich
RT   peptides and of a novel insect defensin.";
RL   J. Insect Physiol. 42:81-89(1996).
CC   -!- FUNCTION: Antibacterial peptide active against Gram-negative
CC       bacteria.
CC   -!- INDUCTION: By bacterial infection.
KW   Antibiotic; Insect immunity.
SQ   SEQUENCE   15 AA;  1893 MW;  23835D063B946299 CRC64;

  Query Match             31.6%;  Score 31;  DB 1;  Length 15;
  Best Local Similarity   62.5%;  Pred. No. 67;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 VEKPDLQP 13
              |:||| :|
Db          1 VDKPDYRP 8


RESULT 3
MK2B_PALPR
ID   MK2B_PALPR     STANDARD;      PRT;    16 AA.
AC   P80410;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Metalnikowin IIB.
OS   Palomena prasina (Green shield bug).
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OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
OC   Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;
OC   Palomena.
OX   NCBI_TaxID=55431;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Hemolymph;
RA   Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
RT   "The inducible antibacterial peptides of the hemipteran insect
RT   Palomena prasina: identification of a unique family of proline-rich
RT   peptides and of a novel insect defensin.";
RL   J. Insect Physiol. 42:81-89(1996).
CC   -!- FUNCTION: Antibacterial peptide active against Gram-negative
CC       bacteria.
CC   -!- INDUCTION: By bacterial infection.
KW   Antibiotic; Insect immunity.
SQ   SEQUENCE   16 AA;  2040 MW;  AF21407D063B9462 CRC64;

  Query Match             31.6%;  Score 31;  DB 1;  Length 16;
  Best Local Similarity   62.5%;  Pred. No. 71;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 VEKPDLQP 13
              |:||| :|
Db          1 VDKPDYRP 8


RESULT 4
MK3_PALPR
ID   MK3_PALPR      STANDARD;      PRT;    16 AA.
AC   P80411;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Metalnikowin III.
OS   Palomena prasina (Green shield bug).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
OC   Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;
OC   Palomena.
OX   NCBI_TaxID=55431;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Hemolymph;
RA   Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
RT   "The inducible antibacterial peptides of the hemipteran insect
RT   Palomena prasina: identification of a unique family of proline-rich
RT   peptides and of a novel insect defensin.";
RL   J. Insect Physiol. 42:81-89(1996).
CC   -!- FUNCTION: Antibacterial peptide active against Gram-negative
CC       bacteria.
CC   -!- INDUCTION: By bacterial infection.
KW   Antibiotic; Insect immunity.
SQ   SEQUENCE   16 AA;  2024 MW;  A9E3835D063B9462 CRC64;

  Query Match             31.6%;  Score 31;  DB 1;  Length 16;
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  Best Local Similarity   62.5%;  Pred. No. 71;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 VEKPDLQP 13
              |:||| :|
Db          1 VDKPDYRP 8


RESULT 5
URE3_MORMO
ID   URE3_MORMO     STANDARD;      PRT;    10 AA.
AC   P17339;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Urease gamma subunit (EC 3.5.1.5) (Urea amidohydrolase gamma subunit)
DE   (Urease 6 kDa subunit) (Fragment).
GN   UREA.
OS   Morganella morganii (Proteus morganii).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Morganella.
OX   NCBI_TaxID=582;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=90264298; PubMed=2345135;
RA   Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT   "Morganella morganii urease: purification, characterization, and
RT   isolation of gene sequences.";
RL   J. Bacteriol. 172:3073-3080(1990).
CC   -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC   -!- SUBUNIT: (Alpha, beta, gamma)(3) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: Belongs to the urease gamma subunit family.
DR   PIR; C35389; C35389.
DR   HAMAP; MF_00739; -; 1.
KW   Hydrolase.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1171 MW;  4B313BCB077771A7 CRC64;

  Query Match             30.6%;  Score 30;  DB 1;  Length 10;
  Best Local Similarity   83.3%;  Pred. No. 61;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 PPDVEK 8
              ||:|||
Db          5 PPEVEK 10


RESULT 6
COXE_THUOB
ID   COXE_THUOB     STANDARD;      PRT;     9 AA.
AC   P80975;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Cytochrome c oxidase polypeptide VIa (EC 1.9.3.1) (Fragment).
OS   Thunnus obesus (Bigeye tuna).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC   Scombridae; Thunnus.
OX   NCBI_TaxID=8241;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Heart;
RX   MEDLINE=97454291; PubMed=9310366;
RA   Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA   Kadenbach B.;
RT   "The subunit structure of cytochrome-c oxidase from tuna heart and
RT   liver.";
RL   Eur. J. Biochem. 248:99-103(1997).
CC   -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC       chains of cytochrome c oxidase, the terminal oxidase in
CC       mitochondrial electron transport.
CC   -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC       c + 2 H(2)O.
CC   -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC   -!- SIMILARITY: Belongs to the cytochrome c oxidase VIa family.
DR   PIR; S77984; S77984.
DR   InterPro; IPR001349; COX6A.
DR   PROSITE; PS01329; COX6A; PARTIAL.
KW   Oxidoreductase; Inner membrane; Mitochondrion.
FT   NON_TER       1      1
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1136 MW;  62E072C9CB0776DB CRC64;

  Query Match             23.5%;  Score 23;  DB 1;  Length 9;
  Best Local Similarity   37.5%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 EKPDLQPF 14
              |:|:  |:
Db          2 EQPEFVPY 9


RESULT 7
PPK4_PERAM
ID   PPK4_PERAM     STANDARD;      PRT;    12 AA.
AC   P82619;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Pyrokinin-4 (Pea-PK-4) (YXPRL-amide).
OS   Periplaneta americana (American cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC   Blattidae; Periplaneta.
OX   NCBI_TaxID=6978;
RN   [1]
RP   SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC   TISSUE=Retrocerebral complex;
RX   MEDLINE=99212469; PubMed=10196736;
RA   Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
RT   "Differential distribution of pyrokinin-isoforms in cerebral and
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RT   abdominal neurohemal organs of the American cockroach.";
RL   Insect Biochem. Mol. Biol. 29:139-144(1999).
RN   [2]
RP   TISSUE SPECIFICITY.
RX   MEDLINE=20189894; PubMed=10723010;
RA   Predel R., Eckert M.;
RT   "Tagma-specific distribution of FXPRLamides in the nervous system of
RT   the American cockroach.";
RL   J. Comp. Neurol. 419:352-363(2000).
CC   -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC       activity).
CC   -!- TISSUE SPECIFICITY: Corpora cardiaca.
CC   -!- MASS SPECTROMETRY: MW=1147.9; METHOD=MALDI.
CC   -!- SIMILARITY: Belongs to the pyrokinin family.
KW   Neuropeptide; Amidation; Pyrokinin.
FT   MOD_RES      12     12       AMIDATION.
SQ   SEQUENCE   12 AA;  1449 MW;  FA7A3049FF42CAA1 CRC64;

  Query Match             22.4%;  Score 22;  DB 1;  Length 12;
  Best Local Similarity   55.6%;  Pred. No. 1.2e+03;
  Matches    5;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 PPDVEKPDL 11
              | ||  | |
Db          4 PHDVYSPRL 12


RESULT 8
TKN2_KASMA
ID   TKN2_KASMA     STANDARD;      PRT;    12 AA.
AC   P08614;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Hylambatin.
OS   Kassina maculata (African rhacophorid frog) (Hylambates maculatus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;
OC   Kassina.
OX   NCBI_TaxID=8414;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RA   Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;
RT   "New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and
RT   hylambatin, in the skin of the African rhacophorid frog Hylambates
RT   maculatus.";
RL   Biomed. Res. 2:613-617(1981).
CC   -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC       evoke behavioral responses, are potent vasodilators and
CC       secretagogues, and contract (directly or indirectly) many smooth
CC       muscles.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
DR   PIR; S07436; S07436.
DR   InterPro; IPR002040; Tachy_Neurokinin.
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DR   Pfam; PF02202; Tachykinin; 1.
DR   PROSITE; PS00267; TACHYKININ; 1.
KW   Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.
FT   MOD_RES      12     12       AMIDATION.
SQ   SEQUENCE   12 AA;  1441 MW;  3287CD2F0DD40AB7 CRC64;

  Query Match             22.4%;  Score 22;  DB 1;  Length 12;
  Best Local Similarity   50.0%;  Pred. No. 1.2e+03;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 PPDVEK 8
              ||| ::
Db          2 PPDPDR 7


RESULT 9
IBP4_PIG
ID   IBP4_PIG       STANDARD;      PRT;    16 AA.
AC   P24854;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)
DE   (IGF-binding protein 4) (Fragment).
GN   IGFBP4.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92109718; PubMed=1722398;
RA   Coleman M.E., Pan Y.-C.E., Etherton T.D.;
RT   "Identification and NH2-terminal amino acid sequence of three
RT   insulin-like growth factor-binding proteins in porcine serum.";
RL   Biochem. Biophys. Res. Commun. 181:1131-1136(1991).
CC   -!- FUNCTION: IGF-binding proteins prolong the half-life of the IGFs
CC       and have been shown to either inhibit or stimulate the growth
CC       promoting effects of the IGFs on cell culture. They alter the
CC       interaction of IGFs with their cell surface receptors.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Contains 1 IGFBP domain.
CC   -!- SIMILARITY: Contains 1 thyroglobulin type-I domain.
DR   PIR; JH0517; JH0517.
DR   InterPro; IPR000867; Insl_gro_fac_pr.
DR   InterPro; IPR000716; Thyroglobulin_1.
DR   PROSITE; PS00222; IGF_BINDING; PARTIAL.
DR   PROSITE; PS00484; THYROGLOBULIN_1; PARTIAL.
KW   Growth factor binding.
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1799 MW;  40988840096655E2 CRC64;

  Query Match             22.4%;  Score 22;  DB 1;  Length 16;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+03;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 PPDVEK 8
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              ||  ||
Db          8 PPSEEK 13


RESULT 10
UF04_MOUSE
ID   UF04_MOUSE     STANDARD;      PRT;     7 AA.
AC   P38642;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Fibroblast;
RX   MEDLINE=95009907; PubMed=7523108;
RA   Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT   "Separation and sequencing of familiar and novel murine proteins
RT   using preparative two-dimensional gel electrophoresis.";
RL   Electrophoresis 15:735-745(1994).
CC   -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC       protein is: 5.0, its MW is: 46 kDa.
FT   NON_TER       7       7
SQ   SEQUENCE   7 AA;  766 MW;  68640AB777632700 CRC64;

  Query Match             21.4%;  Score 21;  DB 1;  Length 7;
  Best Local Similarity   75.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QPPD 5
              :|||
Db          2 KPPD 5


RESULT 11
TKN1_KASMA
ID   TKN1_KASMA     STANDARD;      PRT;    12 AA.
AC   P08613;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Hylambates kassinin ([Glu2,Pro5]kassinin).
OS   Kassina maculata (African rhacophorid frog) (Hylambates maculatus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;
OC   Kassina.
OX   NCBI_TaxID=8414;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RA   Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;
RT   "New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and
RT   hylambatin, in the skin of the African rhacophorid frog Hylambates
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RT   maculatus.";
RL   Biomed. Res. 2:613-617(1981).
CC   -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC       evoke behavioral responses, are potent vasodilators and
CC       secretagogues, and contract (directly or indirectly) many smooth
CC       muscles.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
DR   PIR; S10059; S10059.
DR   InterPro; IPR002040; Tachy_Neurokinin.
DR   InterPro; IPR008215; Tachykinin.
DR   Pfam; PF02202; Tachykinin; 1.
DR   SMART; SM00203; TK; 1.
DR   PROSITE; PS00267; TACHYKININ; 1.
KW   Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.
FT   MOD_RES      12     12       AMIDATION.
SQ   SEQUENCE   12 AA;  1376 MW;  3E756D279DD6DAB7 CRC64;

  Query Match             21.4%;  Score 21;  DB 1;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+03;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 DVEKPD 10
              |  |||
Db          1 DEPKPD 6


RESULT 12
VORA_METTM
ID   VORA_METTM     STANDARD;      PRT;    15 AA.
AC   P80907;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ketoisovalerate oxidoreductase subunit vorA (EC 1.-.-.-) (VOR) (2-
DE   oxoisovalerate oxidoreductase alpha chain) (2-oxoisovalerate-
DE   ferredoxin oxidoreductase alpha subunit) (Fragment).
GN   VORA.
OS   Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC   Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC   Methanobacteriaceae; Methanothermobacter.
OX   NCBI_TaxID=79929;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=97261844; PubMed=9108258;
RA   Tersteegen A., Linder D., Thauer R.K., Hedderich R.;
RT   "Structures and functions of four anabolic 2-oxoacid oxidoreductases
RT   in Methanobacterium thermoautotrophicum.";
RL   Eur. J. Biochem. 244:862-868(1997).
CC   -!- SUBUNIT: HETEROTRIMER OF THE VORA, VORB AND VORC SUBUNITS.
CC   -!- MISCELLANEOUS: Has a pH optimum of 9.7 and an optimal temperature
CC       of 75 degrees Celsius.
KW   Oxidoreductase.
FT   NON_TER      15     15
SQ   SEQUENCE   15 AA;  1779 MW;  31320B6531CA528F CRC64;
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  Query Match             21.4%;  Score 21;  DB 1;  Length 15;
  Best Local Similarity   60.0%;  Pred. No. 2.2e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 VEKPD 10
              : |||
Db          5 IRKPD 9


RESULT 13
SLAP_BACTG
ID   SLAP_BACTG     STANDARD;      PRT;     10 AA.
AC   P49325;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   01-FEB-1996 (Rel. 33, Last annotation update)
DE   S-layer protein (Surface layer protein) (Fragment).
OS   Bacillus thuringiensis (subsp. galleriae).
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=29338;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=NRRL 4045;
RX   MEDLINE=90078111; PubMed=2592346;
RA   Luckevich M.D., Beveridge T.J.;
RT   "Characterization of a dynamic S layer on Bacillus thuringiensis.";
RL   J. Bacteriol. 171:6656-6667(1989).
CC   -!- FUNCTION: The S-layer is a paracrystalline mono-layered assembly
CC       of proteins which coat the surface of bacteria.
CC   -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC       S-LAYER WITH OBLIQUE (P2) SYMMETRY.
DR   PIR; A60476; A60476.
KW   Cell wall; S-layer.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1080 MW;  57AECACAB769D1A3 CRC64;

  Query Match             20.4%;  Score 20;  DB 1;  Length 10;
  Best Local Similarity   60.0%;  Pred. No. 2e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 PDLQP 13
              ||: |
Db          6 PDVXP 10


RESULT 14
UPA2_HUMAN
ID   UPA2_HUMAN     STANDARD;      PRT;     10 AA.
AC   P30088;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Unknown protein from 2D-page of plasma (Spot 10) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
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RN   [1]
RP   SEQUENCE.
RC   TISSUE=Plasma;
RX   MEDLINE=93092937; PubMed=1459097;
RA   Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA   Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA   Hochstrasser D.F.;
RT   "Plasma protein map: an update by microsequencing.";
RL   Electrophoresis 13:707-714(1992).
CC   -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC       protein is: 4.4, its MW is: 49 kDa.
DR   SWISS-2DPAGE; P30088; HUMAN.
FT   NON_TER       1      1
FT   UNSURE        6      6
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1079 MW;  51AC54AAB77775B7 CRC64;

  Query Match             20.4%;  Score 20;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 PPD 5
              |||
Db          5 PPD 7


RESULT 15
MORN_HUMAN
ID   MORN_HUMAN     STANDARD;      PRT;    11 AA.
AC   P01163;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Morphogenetic neuropeptide (Head activator) (HA).
OS   Homo sapiens (Human),
OS   Rattus norvegicus (Rat),
OS   Bos taurus (Bovine),
OS   Anthopleura elegantissima (Sea anemone), and
OS   Hydra attenuata (Hydra) (Hydra vulgaris).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=Human, Rat, and Bovine;
RX   MEDLINE=82035850; PubMed=7290191;
RA   Bodenmuller H., Schaller H.C.;
RT   "Conserved amino acid sequence of a neuropeptide, the head activator,
RT   from coelenterates to humans.";
RL   Nature 293:579-580(1981).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=A.elegantissima, and H.attenuata;
RA   Schaller H.C., Bodenmuller H.;
RT   "Isolation and amino acid sequence of a morphogenetic peptide from
RT   hydra.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
```

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RN   [3]
RP   SYNTHESIS.
RX   MEDLINE=82050803; PubMed=7297679;
RA   Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;
RT   "Synthesis of a new neuropeptide, the head activator from hydra.";
RL   FEBS Lett. 131:317-321(1981).
RN   [4]
RP   FUNCTION.
RX   MEDLINE=90059923; PubMed=2583101;
RA   Schaller H.C., Druffel-Augustin S., Dubel S.;
RT   "Head activator acts as an autocrine growth factor for NH15-CA2 cells
RT   in the G2/mitosis transition.";
RL   EMBO J. 8:3311-3318(1989).
CC   -!- FUNCTION: HA acts as an autocrine growth factor for neural cells
CC       in the G2/mitosis transition.
CC   -!- CAUTION: This peptide was first isolated from nerve cells of hydra
CC       and was called head activator by the authors, because it induced
CC       head-specific growth and differentiation in this animal. It has
CC       been found in mammalian intestine and hypothalamus.
DR   PIR; A01427; YHRT.
DR   PIR; A93900; YHXAE.
DR   PIR; B01427; YHHU.
DR   PIR; B93900; YHJFHY.
DR   PIR; C01427; YHBO.
DR   GK; P01163; -.
KW   Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
SQ   SEQUENCE   11 AA;  1142 MW;  37927417C325B878 CRC64;

  Query Match             20.4%;  Score 20;  DB 1;  Length 11;
  Best Local Similarity   57.1%;  Pred. No. 2.3e+03;
  Matches    4;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 QPPDVEK 8
              |||   |
Db          1 QPPGGSK 7


RESULT 16
XYLA_STRVN
ID   XYLA_STRVN     STANDARD;      PRT;    12 AA.
AC   P14405;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Xylose isomerase (EC 5.3.1.5) (Fragment).
GN   XYLA.
OS   Streptomyces violaceoruber.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1935;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=LMG 7183;
RX   MEDLINE=90104230; PubMed=2604694;
RA   Vangrysperre W., Ampe C., Kersters-Hilderson H., Tempst P.;
RT   "Single active-site histidine in D-xylose isomerase from Streptomyces
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RT   violaceoruber. Identification by chemical derivatization and peptide
RT   mapping.";
RL   Biochem. J. 263:195-199(1989).
CC   -!- CATALYTIC ACTIVITY: D-xylose = D-xylulose.
CC   -!- COFACTOR: Binds 2 magnesium ions per subunit (Potential).
CC   -!- SUBUNIT: Homotetramer.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: Belongs to the xylose isomerase family.
DR   HAMAP; MF_00455; -; 1.
DR   InterPro; IPR001998; Xylose_isom.
DR   PROSITE; PS00172; XYLOSE_ISOMERASE_1; PARTIAL.
DR   PROSITE; PS00173; XYLOSE_ISOMERASE_2; PARTIAL.
KW   Isomerase; Pentose shunt; Xylose metabolism; Metal-binding; Magnesium.
FT   NON_TER       1      1
FT   ACT_SITE      5      5
FT   NON_TER      12     12
SQ   SEQUENCE   12 AA;  1375 MW;  E749268EB1AAAAA1 CRC64;

  Query Match             20.4%;  Score 20;  DB 1;  Length 12;
  Best Local Similarity   80.0%;  Pred. No. 2.5e+03;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 DLQPF 14
              || ||
Db          8 DLIPF 12


RESULT 17
ACT7_SOYBN
ID   ACT7_SOYBN     STANDARD;      PRT;    13 AA.
AC   P15987;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Actin 7 (Fragment).
GN   SAC7.
OS   Glycine max (Soybean).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX   NCBI_TaxID=3847;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Wayne;
RX   MEDLINE=91346640; PubMed=2102831;
RA   Pearson L., Meagher R.B.;
RT   "Diverse soybean actin transcripts contain a large intron in the 5'
RT   untranslated leader: structural similarity to vertebrate muscle actin
RT   genes.";
RL   Plant Mol. Biol. 14:513-526(1990).
CC   -!- FUNCTION: Actins are highly conserved proteins that are involved
CC       in various types of cell motility and are ubiquitously expressed
CC       in all eukaryotic cells.
CC   -!- FUNCTION: Essential component of cell cytoskeleton; plays an
CC       important role in cytoplasmic streaming, cell shape determination,
CC       cell division, organelle movement and extension growth.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
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CC   -!- MISCELLANEOUS: There are at least 16 actin genes in soybean.
CC   -!- SIMILARITY: Belongs to the actin family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X17120; CAA34980.1; -.
DR   PIR; S15755; S15755.
DR   InterPro; IPR004001; Actin.
DR   InterPro; IPR004000; Actin_like.
DR   PROSITE; PS00406; ACTINS_1; PARTIAL.
DR   PROSITE; PS00432; ACTINS_2; PARTIAL.
DR   PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.
KW   Structural protein; Multigene family.
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1420 MW;  8BEFF3C36D4FD05A CRC64;

  Query Match             20.4%;  Score 20;  DB 1;  Length 13;
  Best Local Similarity   75.0%;  Pred. No. 2.7e+03;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 DLQP 13
              |:||
Db          6 DIQP 9


RESULT 18
BRK_PARID
ID   BRK_PARID      STANDARD;      PRT;    13 AA.
AC   P42717;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Waspkinin.
OS   Parapolybia indica.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC   Vespidae; Polistinae; Parapolybia.
OX   NCBI_TaxID=31921;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RA   Toki T., Yasuhara T., Nakajima T.;
RT   "Isolation and sequential analysis of peptides on the venom sac of
RT   Parapolybia indica.";
RL   Eisei Dobutsu 39:105-111(1988).
CC   -!- FUNCTION: Induces smooth muscle contraction.
CC   -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC   -!- SIMILARITY: Belongs to the bradykinin family.
KW   Bradykinin; Vasodilator; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
SQ   SEQUENCE   13 AA;  1573 MW;  2673CB3D83ECC867 CRC64;
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  Query Match             20.4%;  Score 20;  DB 1;  Length 13;
  Best Local Similarity   42.9%;  Pred. No. 2.7e+03;
  Matches    3;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          9 PDLQPFQ 15
              |   ||:
Db          6 PGFSPFR 12


RESULT 19
ECDE_LYMDI
ID   ECDE_LYMDI     STANDARD;      PRT;    13 AA.
AC   P80941;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Testis ecdysiotropin peptide E (TE).
OS   Lymantria dispar (Gypsy moth).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC   Lymantriidae; Lymantria.
OX   NCBI_TaxID=13123;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=97387807; PubMed=9243792;
RA   Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,
RA   Bell R.A.;
RT   "Naturally occurring analogs of Lymantria testis ecdysiotropin, a
RT   gonadotropin isolated from brains of Lymantria dispar pupae.";
RL   Arch. Insect Biochem. Physiol. 36:37-50(1997).
CC   -!- FUNCTION: Stimulates synthesis of ecdysteroid in the testes of
CC       larvae and pupae.
SQ   SEQUENCE   13 AA;  1357 MW;  1841B4CA3275B764 CRC64;

  Query Match             20.4%;  Score 20;  DB 1;  Length 13;
  Best Local Similarity   42.9%;  Pred. No. 2.7e+03;
  Matches    3;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 PDVEKPD 10
              |: : ||
Db          5 PNPDTPD 11


RESULT 20
ACT6_SOYBN
ID   ACT6_SOYBN     STANDARD;      PRT;    17 AA.
AC   P15986;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Actin 6 (Fragment).
GN   SAC6.
OS   Glycine max (Soybean).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
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OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX   NCBI_TaxID=3847;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Wayne;
RX   MEDLINE=91346640; PubMed=2102831;
RA   Pearson L., Meagher R.B.;
RT   "Diverse soybean actin transcripts contain a large intron in the 5'
RT   untranslated leader: structural similarity to vertebrate muscle actin
RT   genes.";
RL   Plant Mol. Biol. 14:513-526(1990).
CC   -!- FUNCTION: Actins are highly conserved proteins that are involved
CC       in various types of cell motility and are ubiquitously expressed
CC       in all eukaryotic cells.
CC   -!- FUNCTION: Essential component of cell cytoskeleton; plays an
CC       important role in cytoplasmic streaming, cell shape determination,
CC       cell division, organelle movement and extension growth.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- MISCELLANEOUS: There are at least 16 actin genes in soybean.
CC   -!- SIMILARITY: Belongs to the actin family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X17119; CAA34979.1; -.
DR   PIR; S15754; S15754.
DR   InterPro; IPR004001; Actin.
DR   InterPro; IPR004000; Actin_like.
DR   PROSITE; PS00406; ACTINS_1; PARTIAL.
DR   PROSITE; PS00432; ACTINS_2; PARTIAL.
DR   PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.
KW   Structural protein; Multigene family.
FT   NON_TER      17     17
SQ   SEQUENCE   17 AA;  1749 MW;  38F4970D4BEFF3C3 CRC64;

  Query Match             20.4%;  Score 20;  DB 1;  Length 17;
  Best Local Similarity   75.0%;  Pred. No. 3.6e+03;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 DLQP 13
              |:||
Db          6 DIQP 9


RESULT 21
PSBL_SYNVU
ID   PSBL_SYNVU     STANDARD;      PRT;    17 AA.
AC   P12241;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Photosystem II reaction center L protein (PSII 5 kDa protein)
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DE   (Fragment).
GN   PSBL.
OS   Synechococcus vulcanus (Thermosynechococcus vulcanus).
OC   Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.
OX   NCBI_TaxID=32053;
RN   [1]
RP   SEQUENCE.
RA   Ikeuchi M., Koike H., Inoue Y.;
RT   "Identification of psbI and psbL gene products in cyanobacterial
RT   photosystem II reaction center preparation.";
RL   FEBS Lett. 251:155-160(1989).
CC   -!- FUNCTION: Not known, it is however required for PSII activity.
CC   -!- SUBCELLULAR LOCATION: Cellular thylakoid membrane.
CC   -!- SIMILARITY: Belongs to the psbL family.
DR   PIR; S05033; S05033.
DR   HAMAP; MF_01317; -; 1.
DR   InterPro; IPR003372; PSII_PsbL.
DR   Pfam; PF02419; PsbL; 1.
KW   Photosynthesis; Thylakoid; Photosystem II; Reaction center.
FT   NON_TER      17     17
SQ   SEQUENCE   17 AA;  2018 MW;  A86FD372B70B9847 CRC64;

  Query Match             20.4%;  Score 20;  DB 1;  Length 17;
  Best Local Similarity   37.5%;  Pred. No. 3.6e+03;
  Matches    3;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          9 PDLQPFQV 16
              |: || ::
Db          5 PNRQPVEL 12


RESULT 22
VESP_VESMC
ID   VESP_VESMC     STANDARD;      PRT;    17 AA.
AC   P57672;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Vespulakinin 1 [Contains: Vespulakinin 2].
OS   Vespula maculifrons (Eastern yellow jacket) (Wasp).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC   Vespidae; Vespinae; Vespula.
OX   NCBI_TaxID=7453;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RX   MEDLINE=76114777; PubMed=1247511;
RA   Yoshida H., Geller R.G., Pisano J.J.;
RT   "Vespulakinins: new carbohydrate-containing bradykinin derivatives.";
RL   Biochemistry 15:61-64(1976).
RN   [2]
RP   SYNTHESIS.
RX   MEDLINE=88057857; PubMed=3679673;
RA   Rocchi R., Biondi L., Filira F., Scolaro B.;
RT   "Synthesis, conformation, and biological activity of the carbohydrate-
RT   free vespulakinin 1.";
```

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RL   Int. J. Pept. Protein Res. 30:240-256(1987).
CC   -!- FUNCTION: Induces smooth muscle contraction.
CC   -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC   -!- SIMILARITY: Belongs to the bradykinin family.
DR   PIR; A61339; A61339.
KW   Bradykinin; Vasodilator; Glycoprotein.
FT   PEPTIDE       1     17       VESPULAKININ 1.
FT   PEPTIDE       3     17       VESPULAKININ 2.
FT   CARBOHYD      3      3       O-LINKED (GALNAC. . .).
FT   CARBOHYD      4      4       O-LINKED (GALNAC. . .).
SQ   SEQUENCE   17 AA;  1960 MW;  58B2CBA864122323 CRC64;

  Query Match             20.4%;  Score 20;  DB 1;  Length 17;
  Best Local Similarity   42.9%;  Pred. No. 3.6e+03;
  Matches    3;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          9 PDLQPFQ 15
              |   ||:
Db         11 PGFSPFR 17


RESULT 23
FIBA_LAMGL
ID   FIBA_LAMGL     STANDARD;      PRT;    18 AA.
AC   P14454;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Lama glama (Llama), and
OS   Lama vicugna (Vicugna) (Vicugna vicugna).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX   NCBI_TaxID=9844, 9843;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=L.glama;
RA   Blomback B., Blomback M., Grondahl N.J.;
RT   "Studies on fibrinopeptides from mammals.";
RL   Acta Chem. Scand. 19:1789-1791(1965).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=L.vicugna;
RA   Mross G.A., Doolittle R.F.;
RT   "Amino acid sequence studies on artiodacty fibrinopeptides.";
RL   Arch. Biochem. Biophys. 122:674-684(1967).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
KW   Blood coagulation; Plasma.
```

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FT   PEPTIDE       1      18       FIBRINOPEPTIDE A.
FT   NON_TER      18      18
SQ   SEQUENCE   18 AA;  1834 MW;  2444487B8B7F4CC6 CRC64;

  Query Match             20.4%;  Score 20;  DB 1;  Length 18;
  Best Local Similarity   60.0%;  Pred. No. 3.8e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 PDVEK 8
              || :|
Db          3 PDADK 7


RESULT 24
BPP3_BOTIN
ID   BPP3_BOTIN     STANDARD;      PRT;    11 AA.
AC   P30423;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting
DE   enzyme inhibitor).
OS   Bothrops insularis (Island jararaca) (Queimada jararaca).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Bothrops.
OX   NCBI_TaxID=8723;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RX   MEDLINE=90351557; PubMed=2386615;
RA   Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT   "Primary structure and biological activity of bradykinin potentiating
RT   peptides from Bothrops insularis snake venom.";
RL   J. Protein Chem. 9:221-227(1990).
CC   -!- FUNCTION: This peptide both inhibits the activity of the
CC       angiotensin-converting enzyme and enhances the action of
CC       bradykinin by inhibiting the kinases that inactivate it.
CC       It acts as an indirect hypotensive agent.
DR   PIR; C37196; C37196.
KW   Hypotensive agent; Pyrrolidone carboxylic acid.
FT   MOD_RES       1       1       PYRROLIDONE CARBOXYLIC ACID.
SQ   SEQUENCE   11 AA;  1199 MW;  20B25813C7741777 CRC64;

  Query Match             19.9%;  Score 19.5;  DB 1;  Length 11;
  Best Local Similarity   36.4%;  Pred. No. 2.7e+03;
  Matches    4;  Conservative    2;  Mismatches    2;  Indels    3;  Gaps    1;

Qy          3 PPDVEKPDLQP 13
              ||   :| : |
Db          4 PP---RPQIPP 11


RESULT 25
BPP4_BOTIN
ID   BPP4_BOTIN     STANDARD;      PRT;    11 AA.
AC   P30424;
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DT   01-APR-1993 (Rel. 25, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting
DE   enzyme inhibitor).
OS   Bothrops insularis (Island jararaca) (Queimada jararaca).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Bothrops.
OX   NCBI_TaxID=8723;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RX   MEDLINE=90351557; PubMed=2386615;
RA   Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT   "Primary structure and biological activity of bradykinin potentiating
RT   peptides from Bothrops insularis snake venom.";
RL   J. Protein Chem. 9:221-227(1990).
CC   -!- FUNCTION: This peptide both inhibits the activity of the
CC       angiotensin-converting enzyme and enhances the action of
CC       bradykinin by inhibiting the kinases that inactivate it.
CC       It acts as an indirect hypotensive agent.
DR   PIR; D37196; D37196.
KW   Hypotensive agent; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
SQ   SEQUENCE   11 AA;  1143 MW;  20BBBF13C7741777 CRC64;

  Query Match             19.9%;  Score 19.5;  DB 1;  Length 11;
  Best Local Similarity   36.4%;  Pred. No. 2.7e+03;
  Matches    4;  Conservative    2;  Mismatches    2;  Indels    3;  Gaps    1;

Qy          3 PPDVEKPDLQP 13
              ||   :| : |
Db          4 PP---RPQIPP 11


RESULT 26
AL12_CARMA
ID   AL12_CARMA     STANDARD;      PRT;     8 AA.
AC   P81815;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Carcinustatin 12.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
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RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC   -!- SIMILARITY: Belongs to the allatostatin family.
KW   Neuropeptide; Multigene family.
SQ   SEQUENCE   8 AA;  913 MW;  672879CDCB569AB7 CRC64;

  Query Match             19.4%;  Score 19;  DB 1;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          9 PDLQPF 14
              ||:  |
Db          1 PDMYAF 6


RESULT 27
KNL3_BOMVA
ID   KNL3_BOMVA     STANDARD;      PRT;      9 AA.
AC   P83058;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   [Thr6]bradykinin.
OS   Bombina variegata (Yellow-bellied toad).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX   NCBI_TaxID=8348;
RN   [1]
RP   SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC   TISSUE=Skin secretion;
RA   Chen T.B., Orr D.F., Bjourson A.J., McClean S., Rao P.F., Shaw C.;
RT   "Cloning and post-translational processing of frog skin kininogens.";
RL   Submitted (JUL-2001) to Swiss-Prot.
CC   -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
CC       arterial smooth muscle and constriction of intestinal smooth
CC       muscle.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
CC   -!- SIMILARITY: Belongs to the bradykinin family.
KW   Amphibian defense peptide; Vasodilator; Bradykinin.
SQ   SEQUENCE   9 AA;  1074 MW;  3393D771A9C86777 CRC64;

  Query Match             19.4%;  Score 19;  DB 1;  Length 9;
  Best Local Similarity   42.9%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          9 PDLQPFQ 15
              |   ||:
Db          3 PGFTPFR 9


RESULT 28
FARP_LOCMI
ID   FARP_LOCMI     STANDARD;      PRT;     10 AA.
AC   P38553;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
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DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   SchistoFLRFamide (PDVDHFLRF-amide) (Cardioexcitatory neuropeptide).
OS   Locusta migratoria (Migratory locust), and
OS   Schistocerca gregaria (Desert locust).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC   Acridoidea; Acrididae; Oedipodinae; Locusta.
OX   NCBI_TaxID=7004, 7010;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=L.migratoria; TISSUE=Brain;
RX   MEDLINE=93324430; PubMed=7687352;
RA   Schoofs L., Holman G.M., Paemen L., Veelaert D., Amelinckx M.,
RA   de Loof A.;
RT   "Isolation, identification, and synthesis of PDVDHFLRFamide
RT   (SchistoFLRFamide) in Locusta migratoria and its association with the
RT   male accessory glands, the salivary glands, the heart, and the
RT   oviduct.";
RL   Peptides 14:409-421(1993).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=S.gregaria; TISSUE=Thoracic nervous system;
RX   MEDLINE=89246543; PubMed=2719702;
RA   Robb S., Packman L.C., Evans P.D.;
RT   "Isolation, primary structure and bioactivity of schistoflrf-amide, a
RT   FMRF-amide-like neuropeptide from the locust, Schistocerca
RT   gregaria.";
RL   Biochem. Biophys. Res. Commun. 160:850-856(1989).
CC   -!- FUNCTION: Muscle inhibiting agent. Involved in the neural control
CC       of the visceral muscles of the heart, accessory glands and
CC       oviduct. May be involved in the regulation of saliva secretion.
CC   -!- TISSUE SPECIFICITY: Found in axons of the male accessory glands,
CC       the salivary glands, the heart, and the oviduct.
CC   -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC       family.
DR   PIR; A32543; A32543.
KW   Neuropeptide; Amidation.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1244 MW;  D3C51729D2C1EAB2 CRC64;

  Query Match             19.4%;  Score 19;  DB 1;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 2.9e+03;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 PDVE 7
              |||:
Db          1 PDVD 4


RESULT 29
BRK_MEGFL
ID   BRK_MEGFL      STANDARD;      PRT;    11 AA.
AC   P12797;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Megascoliakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like
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DE   peptide ([Thr6]bradykinin)].
OS   Megascolia flavifrons (Garden dagger wasp) (Solitary wasp).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC   Scoliidae; Megascolia.
OX   NCBI_TaxID=7437;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RX   MEDLINE=87293024; PubMed=3617088;
RA   Yasuhara T., Mantel P., Nakajima T., Piek T.;
RT   "Two kinins isolated from an extract of the venom reservoirs of the
RT   solitary wasp Megascolia flavifrons.";
RL   Toxicon 25:527-535(1987).
RN   [2]
RP   SEQUENCE.
RC   TISSUE=Venom;
RA   Nakajima T., Piek T., Yashuara T., Mantel P.;
RT   "Two kinins isolated from the venom of Megascolia flavifrons.";
RL   Toxicon 26:34-34(1988).
CC   -!- FUNCTION: Both proteins have bradykinin-like, although lower
CC       activities (e.g. smooth muscle contraction).
CC   -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC   -!- SIMILARITY: Belongs to the bradykinin family.
DR   PIR; B26744; B26744.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0045776; P:negative regulation of blood pressure; ISS.
DR   GO; GO:0045987; P:positive regulation of smooth muscle contra. . .; TAS.
KW   Bradykinin; Vasodilator.
FT   PEPTIDE       1     11       MEGASCOLIAKININ.
FT   PEPTIDE       1      9       BRADYKININ-LIKE PEPTIDE.
SQ   SEQUENCE   11 AA;  1273 MW;  33867393D771A9C8 CRC64;

  Query Match             19.4%;  Score 19;  DB 1;  Length 11;
  Best Local Similarity   42.9%;  Pred. No. 3.2e+03;
  Matches    3;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          9 PDLQPFQ 15
              |   ||:
Db          3 PGFTPFR 9


RESULT 30
TKN_KASSE
ID   TKN_KASSE      STANDARD;      PRT;    12 AA.
AC   P08611;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Kassinin.
OS   Kassina senegalensis (Senegal running frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;
OC   Kassina.
OX   NCBI_TaxID=8415;
RN   [1]
RP   SEQUENCE.
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RC   TISSUE=Skin secretion;
RX   MEDLINE=77246385; PubMed=891753;
RA   Anastasi A., Montecucchi P.C., Erspamer V., Visser J.;
RT   "Amino acid composition and sequence of kassinin, a tachykinin
RT   dodecapeptide from the skin of the African frog Kassina
RT   senegalensis.";
RL   Experientia 33:857-858(1977).
CC   -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC       evoke behavioral responses, are potent vasodilators and
CC       secretagogues, and contract (directly or indirectly) many smooth
CC       muscles.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
DR   PIR; S07206; S07206.
DR   PDB; 1MYU; 16-OCT-02.
DR   InterPro; IPR002040; Tachy_Neurokinin.
DR   Pfam; PF02202; Tachykinin; 1.
DR   PROSITE; PS00267; TACHYKININ; 1.
KW   Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW   3D-structure.
FT   MOD_RES      12     12       AMIDATION.
SQ   SEQUENCE   12 AA;  1336 MW;  91757AB89DD6DAB5 CRC64;

  Query Match             19.4%;  Score 19;  DB 1;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 3.5e+03;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 DVEKPD 10
              || | |
Db          1 DVPKSD 6


RESULT 31
ODPA_CANFA
ID   ODPA_CANFA     STANDARD;      PRT;    13 AA.
AC   P49823;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Pyruvate dehydrogenase E1 component alpha subunit, somatic form
DE   (EC 1.2.4.1) (PDHE1-A type I) (Fragment).
GN   PDHA1.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Heart;
RX   MEDLINE=98163340; PubMed=9504812;
RA   Dunn M.J., Corbett J.M., Wheeler C.H.;
RT   "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT   dog heart proteins.";
RL   Electrophoresis 18:2795-2802(1997).
CC   -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC       conversion of pyruvate to acetyl-CoA and CO(2). It contains
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CC       multiple copies of three enzymatic components: pyruvate
CC       dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC       lipoamide dehydrogenase (E3).
CC   -!- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S-
CC       acetyldihydrolipoamide + CO(2).
CC   -!- COFACTOR: Thiamine pyrophosphate.
CC   -!- ENZYME REGULATION: E1 activity is regulated by phosphorylation
CC       (inactivation) and dephosphorylation (activation) of the alpha
CC       subunit (By similarity).
CC   -!- SUBUNIT: Tetramer of two alpha and two beta subunits.
CC   -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
DR   HSC-2DPAGE; P49823; DOG.
KW   Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
KW   Mitochondrion; Phosphorylation.
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1510 MW;  C97EEBF844085B19 CRC64;

  Query Match             19.4%;  Score 19;  DB 1;  Length 13;
  Best Local Similarity   42.9%;  Pred. No. 3.8e+03;
  Matches    3;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 DVEKPDL 11
              :::| ||
Db          7 EIKKXDL 13


RESULT 32
SRY_URSAR
ID   SRY_URSAR      STANDARD;      PRT;    17 AA.
AC   P36396;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Sex-determining region Y protein (Testis-determining factor)
DE   (Fragment).
GN   SRY OR TDF.
OS   Ursus arctos (Brown bear) (Grizzly bear).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX   NCBI_TaxID=9644;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94214722; PubMed=8162229;
RA   Taberlet P., Mattock H., Dubois-Paganon C., Bouvet J.;
RT   "Sexing free-ranging brown bears Ursus arctos using hairs found in
RT   the field.";
RL   Mol. Ecol. 2:399-403(1993).
CC   -!- FUNCTION: Transcriptional activator which regulates a genetic
CC       switch in male development. It is responsible for initiating male
CC       sex determination. SRY HMG box recognizes DNA by partial
CC       intercalation in the minor groove.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- SIMILARITY: Contains 1 HMG box domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; X74007; CAB37858.1; -.
KW   DNA-binding; Nuclear protein; Transcription regulation; Activator;
KW   Sexual differentiation.
FT   NON_TER       1      1
FT   DNA_BIND     <1     >17       HMG BOX.
FT   NON_TER      17      17
SQ   SEQUENCE   17 AA;  2070 MW;  7385F10073FABA4A CRC64;

  Query Match             19.4%;  Score 19;  DB 1;  Length 17;
  Best Local Similarity   42.9%;  Pred. No. 5e+03;
  Matches    3;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 VEKPDLQ 12
              :| | :|
Db          9 LENPKMQ 15


RESULT 33
BPPB_AGKHA
ID   BPPB_AGKHA     STANDARD;      PRT;    11 AA.
AC   P01021;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Bradykinin-potentiating peptide B (Angiotensin-converting
DE   enzyme inhibitor).
OS   Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Gloydius.
OX   NCBI_TaxID=242054;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RA   Kato H., Suzuki T.;
RT   "Amino acid sequence of bradykinin-potentiating peptide isolated from
RT   the venom of Agkistrodon halys blomhoffii.";
RL   Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).
CC   -!- FUNCTION: This peptide both inhibits the activity of the
CC       angiotensin-converting enzyme and enhances the action of
CC       bradykinin by inhibiting the kinases that inactivate it.
CC       It acts as an indirect hypotensive agent.
DR   PIR; A01254; XASNBA.
KW   Hypotensive agent; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
SQ   SEQUENCE   11 AA;  1199 MW;  295CBF0627741777 CRC64;

  Query Match             18.9%;  Score 18.5;  DB 1;  Length 11;
  Best Local Similarity   36.4%;  Pred. No. 3.8e+03;
  Matches    4;  Conservative    2;  Mismatches    2;  Indels    3;  Gaps    1;

Qy          3 PPDVEKPDLQP 13
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                ||   :| : |
Db            4 PP---RPKIPP 11


RESULT 34
LMT3_LOCMI
ID   LMT3_LOCMI     STANDARD;      PRT;      9 AA.
AC   P41489;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   Locustamyotropin 3 (LOM-MT-3).
OS   Locusta migratoria (Migratory locust).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC   Acridoidea; Acrididae; Oedipodinae; Locusta.
OX   NCBI_TaxID=7004;
RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RC   TISSUE=Brain;
RA   Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA   de Loof A.;
RT   "Isolation, identification and synthesis of locustamyotropin III and
RT   IV, two additional neuropeptides of Locusta migratoria: members of the
RT   locustamyotropin peptide family.";
RL   Insect Biochem. Mol. Biol. 22:447-452(1992).
CC   -!- FUNCTION: Potent mediator of visceral muscle contractile activity
CC       (myotropic activity).
CC   -!- SIMILARITY: Belongs to the pyrokinin family.
DR   PIR; A61620; A61620.
DR   InterPro; IPR001484; Pyrokinin.
DR   PROSITE; PS00539; PYROKININ; 1.
KW   Neuropeptide; Amidation; Pyrokinin.
FT   MOD_RES       9      9       AMIDATION.
SQ   SEQUENCE   9 AA;  1140 MW;  D5AE1772C9D776C6 CRC64;

  Query Match             18.4%;  Score 18;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 QPF 14
              |||
Db          3 QPF 5


RESULT 35
FAR6_PANRE
ID   FAR6_PANRE     STANDARD;      PRT;     10 AA.
AC   P82660;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   FMRFamide-like neuropeptide PF6 (NGAPQPFVRF-amide).
OS   Panagrellus redivivus.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC   Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX   NCBI_TaxID=6233;
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RN   [1]
RP   SEQUENCE, FUNCTION, AND AMIDATION.
RA   Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
RA   Maule A.G.;
RT   "Isolation, characterization and pharmacology of RMRFamide-related
RT   peptides (FaRPs) from free-living nematode, Panagrellus redivivus.";
RL   Submitted (JUL-2000) to Swiss-Prot.
CC   -!- FUNCTION: Myoactive.
CC   -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC       family.
KW   Neuropeptide; Amidation.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1132 MW;  CB13E4C9D776C76D CRC64;

  Query Match             18.4%;  Score 18;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 QPF 14
              |||
Db          5 QPF 7


RESULT 36
FARI_CALVO
ID   FARI_CALVO     STANDARD;      PRT;    12 AA.
AC   P41869;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   CalliMIRFamide 1.
OS   Calliphora vomitoria (Blue blowfly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC   Calliphoridae; Calliphora.
OX   NCBI_TaxID=27454;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Thoracic ganglion;
RX   MEDLINE=92196111; PubMed=1549595;
RA   Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA   Rehfeld J.F., Thorpe A.;
RT   "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT   neuropeptides (designated calliFMRFamides) from the blowfly
RT   Calliphora vomitoria.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC   -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC       family.
DR   PIR; E44787; E44787.
KW   Neuropeptide; Amidation.
FT   MOD_RES      12     12       AMIDATION.
SQ   SEQUENCE   12 AA;  1390 MW;  2DDDB316914AB5A7 CRC64;

  Query Match             18.4%;  Score 18;  DB 1;  Length 12;
  Best Local Similarity   60.0%;  Pred. No. 4.9e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          1 DQPPD 5
              :|| |
Db          3 NQPSD 7


RESULT 37
HS9A_RAT
ID   HS9A_RAT       STANDARD;      PRT;    12 AA.
AC   P82995;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Heat shock protein HSP 90-alpha (Fragment).
GN   HSPCA.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=Sprague-Dawley; TISSUE=Liver;
RX   MEDLINE=21589773; PubMed=11732320;
RA   Langer T., Fasold H.;
RT   "Isolation and quantification of the heat shock protein 90 alpha and
RT   beta isoforms from rat liver.";
RL   Protoplasma 218:54-56(2001).
CC   -!- FUNCTION: Molecular chaperone. Has ATPase activity (By
CC       similarity).
CC   -!- SUBUNIT: Homodimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: Belongs to the heat shock protein 90 family.
DR   InterPro; IPR001404; Hsp90.
DR   PROSITE; PS00298; HSP90; PARTIAL.
KW   Chaperone; ATP-binding; Heat shock; Phosphorylation.
FT   MOD_RES       4       4       PHOSPHORYLATION (BY DS-DNA KINASE) (BY
FT                                 SIMILARITY).
FT   MOD_RES       6       6       PHOSPHORYLATION (BY DS-DNA KINASE) (BY
FT                                 SIMILARITY).
FT   NON_TER      12      12
SQ   SEQUENCE   12 AA;  1432 MW;  DE47C322CAB6C1B6 CRC64;

  Query Match             18.4%;  Score 18;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DQP 3
              |||
Db          8 DQP 10


RESULT 38
EP65_HUMAN
ID   EP65_HUMAN     STANDARD;      PRT;    13 AA.
AC   P54963;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
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DE   Erythrocyte 65 kDa protein (P65) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE.
RX   MEDLINE=90004678; PubMed=2507249;
RA   Hart G.W., Haltiwanger R.S., Holt G.D., Kelly W.G.;
RT   "Nucleoplasmic and cytoplasmic glycoproteins.";
RL   Ciba Found. Symp. 145:102-118(1989).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
DR   GO; GO:0005737; C:cytoplasm; NAS.
KW   Glycoprotein.
FT   NON_TER       1      1
FT   CARBOHYD      2      2       O-LINKED (GLCNAC).
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1300 MW;  D0B873344C61A776 CRC64;

  Query Match             18.4%;  Score 18;  DB 1;  Length 13;
  Best Local Similarity   45.5%;  Pred. No. 5.4e+03;
  Matches    5;  Conservative    1;  Mismatches    3;  Indels    2;  Gaps    1;

Qy          1 DQPPDVEKPDL 11
              | |  | :| |
Db          1 DSP--VSQPSL 9


RESULT 39
PEDI_HYDAT
ID   PEDI_HYDAT     STANDARD;      PRT;    13 AA.
AC   P80578;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Pedin.
OS   Hydra attenuata (Hydra) (Hydra vulgaris).
OC   Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC   Hydridae; Hydra.
OX   NCBI_TaxID=6087;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=96232307; PubMed=8674432;
RA   Hoffmeister S.A.H.;
RT   "Isolation and characterization of two new morphogenetically active
RT   peptides from Hydra vulgaris.";
RL   Development 122:1941-1948(1996).
CC   -!- FUNCTION: Morphogenetically active peptide. Active in foot
CC       development.
KW   Morphogen.
SQ   SEQUENCE   13 AA;  1512 MW;  6F5266E3F37632CB CRC64;

  Query Match             18.4%;  Score 18;  DB 1;  Length 13;
  Best Local Similarity   60.0%;  Pred. No. 5.4e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 PDVEK 8
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              ||| :
Db          9 PDVSE 13


RESULT 40
TY13_PHYRO
ID   TY13_PHYRO     STANDARD;      PRT;    13 AA.
AC   P04096;
DT   01-NOV-1986 (Rel. 03, Created)
DT   01-NOV-1986 (Rel. 03, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Tryptophyllin-13.
OS   Phyllomedusa rohdei (Rohde's leaf frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC   Phyllomedusinae; Phyllomedusa.
OX   NCBI_TaxID=8394;
RN   [1]
RP   SEQUENCE.
RA   Montecucchi P.C., Gozzini L., Erspamer V.;
RT   "Primary structure determination of a tryptophan-containing
RT   tridecapeptide from Phyllomedusa rohdei.";
RL   Int. J. Pept. Protein Res. 27:175-182(1986).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
DR   PIR; A05174; A05174.
KW   Amphibian defense peptide; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
SQ   SEQUENCE   13 AA;  1646 MW;  33BF33A212227773 CRC64;

  Query Match             18.4%;  Score 18;  DB 1;  Length 13;
  Best Local Similarity   57.1%;  Pred. No. 5.4e+03;
  Matches    4;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 EKPDLQP 13
              |||   |
Db          2 EKPYWPP 8


RESULT 41
MARI_ALTSP
ID   MARI_ALTSP     STANDARD;      PRT;    14 AA.
AC   P29399;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Marinostatin C-2 [Marinostatin C-1; Marinostatin D].
OS   Alteromonas sp. (strain B-10-31).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC   Alteromonadaceae; Alteromonas.
OX   NCBI_TaxID=29456;
RN   [1]
RP   SEQUENCE, AND ACTIVE SITE.
RX   MEDLINE=92176155; PubMed=1794974;
RA   Takano R., Imada C., Kamei K., Hara S.;
RT   "The reactive site of marinostatin, a proteinase inhibitor from
RT   marine Alteromonas sp. B-10-31.";
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RL   J. Biochem. 110:856-858(1991).
CC   -!- FUNCTION: INHIBITS SUBTILISIN, CHYMOTRYPSIN, AND ELASTASE, BUT
CC       NOT TRYPSIN.
KW   Serine protease inhibitor; Pyrrolidone carboxylic acid.
FT   PEPTIDE       1     14       MARINOSTATIN C-2.
FT   PEPTIDE       3     14       MARINOSTATIN C-1.
FT   PEPTIDE       4     14       MARINOSTATIN D.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   ACT_SITE      6      7       REACTIVE BOND.
SQ   SEQUENCE   14 AA;  1644 MW;  6E7CEEF92EF32E44 CRC64;

  Query Match             18.4%;  Score 18;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 QPF 14
              |||
Db          1 QPF 3


RESULT 42
HS11_PINPS
ID   HS11_PINPS     STANDARD;      PRT;    15 AA.
AC   P81083;
DT   15-JUL-1998 (Rel. 36, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Probable class I heat shock protein (Water stress responsive protein
DE   3) (Fragment).
OS   Pinus pinaster (Maritime pine).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX   NCBI_TaxID=71647;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Needle;
RX   MEDLINE=98418576; PubMed=9747804;
RA   Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;
RT   "Water-deficit-responsive proteins in maritime pine.";
RL   Plant Mol. Biol. 38:587-596(1998).
RN   [2]
RP   SEQUENCE.
RC   TISSUE=Needle;
RX   MEDLINE=99274088; PubMed=10344291;
RA   Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA   Frigerio J.-M., Plomion C.;
RT   "Separation and characterization of needle and xylem maritime pine
RT   proteins.";
RL   Electrophoresis 20:1098-1108(1999).
RN   [3]
RP   REVISION TO 1.
RA   Frigerio J.-M.;
RL   Submitted (SEP-2001) to Swiss-Prot.
CC   -!- SUBUNIT: Forms oligomeric structures (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- INDUCTION: By water stress.
CC   -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein
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CC       (spot N144) is: 6.1, its MW is: 17 kDa.
CC   -!- SIMILARITY: Belongs to the small heat shock protein (HSP20)
CC       family.
CC   -!- SIMILARITY: PLANTS HAVE FOUR CLASSES OF HSP20: CLASS I AND II
CC       WHICH ARE CYTOPLASMIC; CLASS III WHICH IS IN THE CHLOROPLAST
CC       AND CLASS IV WHICH IS IN THE ENDOMEMBRANE. THIS PROTEIN BELONGS
CC       TO CLASS I.
DR   InterPro; IPR002068; Hsp20.
DR   PROSITE; PS01031; HSP20; PARTIAL.
KW   Heat shock; Multigene family.
FT   NON_TER       1      1
FT   NON_TER      15     15
SQ   SEQUENCE   15 AA;  1847 MW;  87FC504C2EB1F2B7 CRC64;

  Query Match             18.4%;  Score 18;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 PFQ 15
              |||
Db         12 PFQ 14


RESULT 43
PSAO_CUCSA
ID   PSAO_CUCSA     STANDARD;      PRT;    15 AA.
AC   P42052;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Photosystem 1 reaction centre subunit 8 (Photosystem I 17.5 kDa
DE   protein) (Fragment).
GN   PSAM.
OS   Cucumis sativus (Cucumber).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX   NCBI_TaxID=3659;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cotyledon;
RX   MEDLINE=91355209; PubMed=1883835;
RA   Iwasaki Y., Ishikawa H., Hibino T., Takabe T.;
RT   "Characterization of genes that encode subunits of cucumber PS I
RT   complex by N-terminal sequencing.";
RL   Biochim. Biophys. Acta 1059:141-148(1991).
CC   -!- FUNCTION: Essential for the activity of NADP photoreduction.
DR   PIR; E56819; E56819.
KW   Photosystem I; Photosynthesis; Chloroplast; Thylakoid; Membrane.
FT   NON_TER      15     15
SQ   SEQUENCE   15 AA;  1714 MW;  CA0BF5DAD403D9F4 CRC64;

  Query Match             18.4%;  Score 18;  DB 1;  Length 15;
  Best Local Similarity   57.1%;  Pred. No. 6.2e+03;
  Matches    4;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 DLQPFQV 16
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              |   |||
Db          4 DXPTFQV 10


RESULT 44
UC23_MAIZE
ID   UC23_MAIZE     STANDARD;      PRT;    15 AA.
AC   P80629;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Unknown protein from 2D-page of etiolated coleoptile (Spot 502)
DE   (Fragment).
OS   Zea mays (Maize).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX   NCBI_TaxID=4577;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Coleoptile;
RA   Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA   Pernollet J.-C., Zivy M., de Vienne D.;
RT   "The maize two dimensional gel protein database: towards an integrated
RT   genome analysis program.";
RL   Theor. Appl. Genet. 93:997-1005(1996).
CC   -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC       protein is: 6.2, its MW is: 45.0 kDa.
DR   Maize-2DPAGE; P80629; COLEOPTILE.
DR   MaizeDB; 123955; -.
FT   NON_TER       1      1
FT   NON_TER      15     15
SQ   SEQUENCE   15 AA;  1557 MW;  C974ED33E9A4EC28 CRC64;

  Query Match             18.4%;  Score 18;  DB 1;  Length 15;
  Best Local Similarity   60.0%;  Pred. No. 6.2e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DQPPD 5
              |:| |
Db          3 DKPGD 7


RESULT 45
LPK1_LOCMI
ID   LPK1_LOCMI     STANDARD;      PRT;    16 AA.
AC   P20404;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Locustapyrokinin 1 (LOM-PK-1).
OS   Locusta migratoria (Migratory locust).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC   Acridoidea; Acrididae; Oedipodinae; Locusta.
OX   NCBI_TaxID=7004;
RN   [1]
```

```
RP   SEQUENCE.
RC   TISSUE=Corpora cardiaca;
RX   MEDLINE=91224474; PubMed=2026322;
RA   Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT   "Isolation, primary structure, and synthesis of locustapyrokinin: a
RT   myotropic peptide of Locusta migratoria.";
RL   Gen. Comp. Endocrinol. 81:97-104(1991).
CC   -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC       activity).
CC   -!- SIMILARITY: Belongs to the pyrokinin family.
DR   PIR; A49761; A49761.
DR   InterPro; IPR001484; Pyrokinin.
DR   PROSITE; PS00539; PYROKININ; 1.
KW   Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      16     16       AMIDATION.
SQ   SEQUENCE   16 AA;  1827 MW;  A7178BBDCA0AFDD6 CRC64;

  Query Match             18.4%;  Score 18;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 6.7e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 QPF 14
              |||
Db         10 QPF 12


RESULT 46
LCTN_LAMGL
ID   LCTN_LAMGL     STANDARD;      PRT;     18 AA.
AC   P83315;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Lactophorin (Whey protein) (Fragment).
OS   Lama glama (Llama).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX   NCBI_TaxID=9844;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=20000588; PubMed=10531593;
RA   Kappeler S., Farah Z., Puhan Z.;
RT   "Alternative splicing of lactophorin mRNA from lactating mammary gland
RT   of the camel (Camelus dromedarius).";
RL   J. Dairy Sci. 82:1-10(1999).
CC   -!- SIMILARITY: Belongs to the PP3 / GlyCAM-1 family.
DR   GO; GO:0005576; C:extracellular; ISS.
DR   InterPro; IPR007906; GLYCAM-1.
DR   Pfam; PF05242; GLYCAM-1; 1.
FT   NON_TER      18     18
SQ   SEQUENCE   18 AA;  2079 MW;  CD59616E5B236AC6 CRC64;

  Query Match             18.4%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   30.8%;  Pred. No. 7.5e+03;
  Matches    4;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;
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Qy          1 DQPPDVEKPDLQP 13
              ::| |    : ||
Db          6 NEPKDEIYMESQP 18


RESULT 47
BPP2_BOTJA
ID   BPP2_BOTJA     STANDARD;      PRT;    10 AA.
AC   P01022;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme
DE   inhibitor V-6-II).
OS   Bothrops jararaca (Jararaca).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Bothrops.
OX   NCBI_TaxID=8724;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RX   MEDLINE=72118526; PubMed=4334402;
RA   Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
RA   Kocy O.;
RT   "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
RT   jararaca. Isolation, elucidation of structure, and synthesis.";
RL   Biochemistry 10:4033-4039(1971).
CC   -!- FUNCTION: This peptide both inhibits the activity of the
CC       angiotensin-converting enzyme and enhances the action of
CC       bradykinin by inhibiting the kinases that inactivate it.
CC       It acts as an indirect hypotensive agent.
DR   PIR; A01255; XAVI6B.
KW   Hypotensive agent; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
SQ   SEQUENCE   10 AA;  1232 MW;  30C53546C7741773 CRC64;

  Query Match             17.3%;  Score 17;  DB 1;  Length 10;
  Best Local Similarity   33.3%;  Pred. No. 5.8e+03;
  Matches    2;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 KPDLQP 13
              :| : |
Db          5 RPQIPP 10


RESULT 48
BPP8_BOTIN
ID   BPP8_BOTIN     STANDARD;      PRT;    10 AA.
AC   P30426;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Bradykinin-potentiating peptide S5,1 (Angiotensin-converting
DE   enzyme inhibitor).
OS   Bothrops insularis (Island jararaca) (Queimada jararaca).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Bothrops.
OX   NCBI_TaxID=8723;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RX   MEDLINE=90351557; PubMed=2386615;
RA   Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT   "Primary structure and biological activity of bradykinin potentiating
RT   peptides from Bothrops insularis snake venom.";
RL   J. Protein Chem. 9:221-227(1990).
CC   -!- FUNCTION: This peptide both inhibits the activity of the
CC       angiotensin-converting enzyme and enhances the action of
CC       bradykinin by inhibiting the kinases that inactivate it.
CC       It acts as an indirect hypotensive agent.
DR   PIR; H37196; H37196.
KW   Hypotensive agent; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
SQ   SEQUENCE   10 AA;  1173 MW;  2FF835545761F6D8 CRC64;

  Query Match             17.3%;  Score 17;  DB 1;  Length 10;
  Best Local Similarity   28.6%;  Pred. No. 5.8e+03;
  Matches    2;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 EKPDLQP 13
              : |:: |
Db          4 QHPNIPP 10


RESULT 49
EFG_CLOPA
ID   EFG_CLOPA      STANDARD;      PRT;    11 AA.
AC   P81350;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Elongation factor G (EF-G) (CP 5) (Fragment).
GN   FUSA.
OS   Clostridium pasteurianum.
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1501;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=W5;
RX   MEDLINE=98291870; PubMed=9629918;
RA   Flengsrud R., Skjeldal L.;
RT   "Two-dimensional gel electrophoresis separation and N-terminal
RT   sequence analysis of proteins from Clostridium pasteurianum W5.";
RL   Electrophoresis 19:802-806(1998).
CC   -!- FUNCTION: This protein promotes the GTP-dependent translocation of
CC       the nascent protein chain from the A-site to the P-site of the
CC       ribosome.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC       EF-G/EF-2 subfamily.
DR   InterPro; IPR000795; EF_GTPbind.
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DR   PROSITE; PS00301; EFACTOR_GTP; PARTIAL.
KW   Elongation factor; Protein biosynthesis; GTP-binding.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1337 MW;  412E71F1D9C33B17 CRC64;

  Query Match             17.3%;  Score 17;  DB 1;  Length 11;
  Best Local Similarity   50.0%;  Pred. No. 6.4e+03;
  Matches    4;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          8 KPDLQPFQ 15
              |  |: ||
Db          1 KYPLEKFQ 8


RESULT 50
RRPL_CHAV
ID   RRPL_CHAV      STANDARD;      PRT;    11 AA.
AC   P13179;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
DE   (L protein) (Fragment).
GN   L.
OS   Chandipura virus (strain I653514).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Rhabdoviridae; Vesiculovirus.
OX   NCBI_TaxID=11273;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89299473; PubMed=2741347;
RA   Masters P.S., Bhella R.S., Butcher M., Patel B., Ghosh H.P.,
RA   Banerjee A.K.;
RT   "Structure and expression of the glycoprotein gene of Chandipura
RT   virus.";
RL   Virology 171:285-290(1989).
CC   -!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
CC       POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS
CC       METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.
CC   -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC       {RNA}(N).
CC   -!- SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE
CC       NUCLEOCAPSID (N) PROTEIN.
CC   -!- SIMILARITY: WITH THE L PROTEIN OF OTHER RHABDOVIRUSES AND
CC       PARAMYXOVIRUSES.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J04350; AAA42917.1; -.
KW   Transferase; RNA-directed RNA polymerase.
FT   NON_TER      11     11
```

SQ SEQUENCE 11 AA; 1189 MW; 0335D6E3AAB2D764 CRC64;

Query Match 17.3%; Score 17; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          10 DLQP 13
               || |
Db           2 DLNP 5
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Search completed: July 4, 2004, 04:41:27
Job time : 7.1791 secs